```
A;Cross-references: UNIPROT:P19761; UNIPARC:UPI000016C61D; GB:861902; NID:g386015; C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhib; F;49-99/Domain: animal Kunitz-type proteinase inhibitor homology <BPI1> P;120-170/Domain: animal Kunitz-type proteinase inhibitor homology <BPI> P;120-170/Domain: animal Kunitz-type proteinase inhibitor homology <BPI> F;212-262/Domain: animal Kunitz-type proteinase inhibitor homology <BPI2>
tissue factor pathway inhibitor precursor [validated] - human N_iAlternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation
                                                                                                                                                                                                                                                                        S
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R;Belaaouaj, A.; Kuppuswamy, M.N.; Birktoft, J.J.; Bajaj, S.P.
Thromb. Res. 69, 547-553, 193
A;Title: Revised cDNA sequence of rabbit tissue factor pathway
A;Reference number: I46937; MUID:93276427; PMID:8503123
A;Accession: I46937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue factor pathway inhibitor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Residues: 1-299 <BEL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLLFLTEAALGDAAQEPTGNNA------EICLLPLDYGPCRALLLRYYYDRYTQ 59
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                                                                                                                                                                                       TYTGCGGNDNNFVSREDCKRACAKAL------KKKKKMP 219
                                                                                                                                                                                                                                   DHRTQLNTVNNTLINQPTKAPRRWAFHGPSWCLPPADRGLCQANBIRFFYNAIIGKCRPF
                                                                                                                                                                                                                                                                                                                                                                          VSVDDQCEGSTEKYFFNLSSMTCEKFFSGGCHRNRIENRFPDEATCMGFC-----
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                                                                                                                                         KYSGCGGNENNFTSKKACITACKKGFIRNLSKGGLIKTKRKKKKQP
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100.0%; Pred. No. 3.2e-110;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                  --APKKI----PSFCYSPKDEGLCSANVTRYYFNPRYRTCDAF 186
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A;Cross-references: UNIPARC:UPI0000136C8F
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C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 09-Jul-2004
C;Accession: A23712; A33716; Ā28650; A60433; B60433; S13\overline{0}34; A34315; A38294; S0390:
R;Girard, T.J.; Eddy, R.; Wesselschmidt, R.L.; MacPhail, L.A.; Likert, K.M.; Byers,
J. Biol. Chem. 266, 5036-5041, 1991
A;Title: Structure of the human lipoprotein-associated coagulation inhibitor gene.
A;Reference number: A23712; MUID:91161593; PMID:2002045
A; Accession: A237:
                                                                                                                                                                                  S03903
Byers, M.G.;
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A;Cross-references: UNIPROT:P10646; UNIPARC:UPI0000136C8F; R;van der Logt, C.P.B.; Reitsma, P.H.; Bertina, R.M. Biochemistry 30, 1571-1577, 1991 GB:M59493; GB:M59499; NID:g187

A;Title: Intron-exon organization of the human gene coding A;Reference number: A39176; MUID:91129227; PMID:1993173 A;Accession: A39176 for the lipoprotein-associated

PIDN: AAA594

õ

A;Cross-references: UNIPARC:UPI0000136C8F; GB:J03225; NID:g180545; PIDN:AAA52022.1; PID: A;Note: part of this sequence, including the amino end of the mature protein, was confirm R;Girard, T.J.; Warren, L.A.; Novotny, W.F.; Bejcek, B.E.; Miletich, J.P.; Broze Jr., G.; Thromb. Res. 55, 37-50, 1989

R;Girard, T.J.; Warren, L.A.; Novotny, W.F.; Bejcek, B.E.; Miletich, J.P.; Broze Jr., G. Thromb. Res. 55, 37-50, 1999
A;Title: Identification of the 1.4 KB and 4.0 KB messages for the lipoprotein associated A;Reference number: A60433; MUID:89388722; PMID:2781520
A;Accession: A60433

A; Molecule type: mRNA A; Status: not compared with conceptual translation

A, Experimental source: endothelial cells

A;Molecule type: protein
A;Residues: 'XX',31-53,'X',55-56 <GI3>
A;Cross-references: UNIPARC:UPI0000173151

A;Experimental source: recombinant material from mouse C137 cells R;Girard, T.J.; McCourt, D.; Novotny, W.F.; MacPhail, L.A.; Likert, Biochem. J. 270, 621-625, 1990
A;Title: Endogenous phosphorylation of the lipoprotein-associated co A;Reference number: S13034; MUID:91054349; PMID:2122883 K.M.; Broze Jr., G.J.

lipoprotein-associated coagulation inhibitor &

A; Accession: S13034

A; Molecule type: protein A; Residues: 29-35 < GI4>

A;Cross-references: UNIPARC:UPI0000173152

G.J.

R;Novotny, W.P.; Girard, T.J.; Miletich, J.P.; Broze Jr., J. Biol. Chem. 264, 18832-18837, 1999
A;Title: Purification and characterization of the lipoprol A;Title: number: A34315; MUID:90036996; PMID:2553722 of the lipoprotein-associated PMID:2553722

coagulation

inhi

A; Accession: A34315

A;Molecule type: protein
A;Residues: 'XX',31-33,'L',35-50 <NOV>
A;Cross-references: UNIPARC:UPI0000173153

A,Experimental source: plasma
R,Pedersen, A.H.; Nordfang, O.; Norris, F.; Wiberg, F.C
J. Biol. Chem. 265, 16786-16793, 1990
A,Title: Recombinant human extrinsic pathway inhibitor.
A,Reference number: A38294, MUID:91009092; PMID:2211593
A,Accession: A38294 F.C.; Christensen, P.M.; Moeller, K.E

Production,

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R;Girard, T.J.; Warren, L. Nature 338, 518-520, 1989 domains of lipoprotein-ass S.G.; Miletich,

A;Title: Functional significance of the Kunitz-type inhibitory A;Reference number: S03903; MUID:89181950; PMID:2927510 A;Contents: annotation; site-directed mutagenesis

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Scoring table:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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1306
1 MDPARPLGL6ILLLFLTEAA.....KKMPKLRFAGRIRKIRKKQF 235
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

hypothetical prote inter-alpha-trypsi	117071		1000		ا د
	2 A29652	123	15.0	196	28
	2 T20219	228	15.1	197	27
	2 T32980	692	15.2	199	26
	2 T21275	1203	15.8	206	25
alpha-1-microglobu	1 TIBOBI	352	16.4	214	24
hypothetical prote	2 T27822	1208	16.5	215	23
hepatocyte growth	2 JG0185	252	16.5	215	22
hypothetical prote	2 T20125	838	18.3	239	21
	2 T20406	1391	18.4	240	20
		1743	19.3	252	19
	2 T19734	1043	19.4	253.5	18
•	2 T16210	1599	20.5	268	17
	2 D88550	1474	20.5	268	16
ď	2 S28291	2844	20.8	271.5	15
protein ZC84.1 [im	2 E88550	1416	20.8	271.5	14
protein T22F7.3 [i	2 Н88380		21.4	279.5	13
hypothetical prote	2 T23573	922	21.8	285	12
	2 C89114	1558	22.4	292.5	11
hypothetical prote	2 T33216	1965	22.9	299	10
	2 T34395	2167	23.2	303	9
	2 T26063	2225	23.4	305.5	8
Ř	2 853325	396	26.5	346.5	7
lipoprotein-associ	2 \$12143	300	28.5	372.5	o
tissue factor path	1 TIRTGK	302	28.8	376	s
tissue factor path	1 JC2264	304	29.4	384.5	4
tissue factor path	1 TIHUGK	304	29.7	388	ω
tissue factor path	2 I46937	299	29.9	390	N
	2 A54951	235	100.0	1306	–
Description	B ID	ength DB	Match Length	Score	No.
			Query		Result

F;96-149/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>

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163	164	165	165.5	166.5	168	172	173	174	178.5	180	182.5	184.5	186	186	188
12.5	12.6	12.6	12.7	12.7	12.9	13.2	13.2	13.3	13.7	13.8	14.0	14.1	14.2	14.2	14.4
57	265	65	110	372	62	62	335	51	502	352	355	349	349	125	183
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A59204	A53390	TIVIVC	TITTOR	JC2556	S07451	819327	T32657	TIVIT1	T20130	HCHU	S22181	835708	S21089	IHOBI	T28711
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ALIGNMENTS

RESULT 1 A54951 tissue factor pathway inhibitor-2 precursor - human tissue factor pathway inhibitor-2 precursor - human N;Alternate names: placental protein 5 (PP5) C;Species: Homo sapiens (man)
C;Accession: A54951; I55185; A34029; C34029; B34029 R;Sprocher; C.A.; Kisiel, W.; Mathewes, S.; Foster, D.C. PTOC, Natl. Acad. Sci. U.S.A. 91, 3353-3357, 1994 A;Title: Molecular Cloning, expression, and partial characterization of a sA;Reference number: A54951; MUID:94211862; PMID:8159751 A;Accession: A54951 A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-235 <res> A;Residues: 1-235 <res> A;Cross-references: UNIPROT:P48307; UNIPARC:UPI00000362E2; GB:L27624; NID:g441149; PIDN:I</res></res>
A;Experimental Bource: placenta R;Miyagi, Y.; Koshikawa, N.; Yasumitsu, H.; Miyagi, B.; Hirahara, F.; Aoki, I.; Misugi, F Blochem_116. 939-942, 1994 A;TITLE: CDNA cloning and mRNA expression of a serine proteinase inhibitor secreted by Ct A;Reference number: I55185; MUID:95204397; PMID:7896752
A; Ctacus: nucleic acid sequence not shown; translation not shown; translated from GB/EMBI A; Molecule type: mRNA A; Residues: 1-235 < RE2> A; Cross-references: UNIPARC:UPI00000362E2; GB:D29992; NID:9484050; PIDN:BAA06272.1; PID:9
R; Buetzow, R; Huhtala; M.L.; Bohn, H.; Virtanen, I.; Seppaelae, M. Biochem. Biophys. Res. Commun. 150, 483-490, 1988 A; Title: Purification and characterization of placental protein 5. A; Reference number: A34029; MUID:88106628; PMID:3276312
A;Accession: A34029 A;Molecule type: protein A;Residues: 'A',24-33,'X',35 <bue> A;Cross-references: UNIPARC:UPI00001762A7 A:Accession: C34029</bue>
A;Accession: C34029 A;Molecule type: protein A;Residues: 47-50, 'X', 52-53 <bu2> A;Cross-references: UNIPARC:UPI00001762A7 A;Accession: B34029 A;Accession: B34029</bu2>
A; Molecule type: protein A; Residues: 133,'X',135-137,'X',139-140,'X',142-144,'X',146 <bu3> A; Cross-references: UNIPARC:UPIO0001762A7 C; Genetics: A; Gene: GDB:TFPI2</bu3>
A; Gene: GDB: IFF12 A; Cross-references: GDB:354485 A; Cross-references: GDB:354485 C; Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor the C; Keywords: anticoagulant; blood coagulation; duplication; glycoprotein; heparin binding; C; Keywords: airicoagulant; blood coagulation; duplication; glycoprotein; heparin binding; F; 1-22/Domain: signal sequence #status predicted <sig-f; #status="" 1-23="" 23-235="" <mat="" <sig-f;="" domain:="" factor="" inhibitor-2="" pathway="" predicted="" product:="" sequence="" signal="" tissue=""> F; 23-235/Product: tissue factor pathway inhibitor-2 #status predicted <mat></mat></sig-f;>
F;36-86/Domain: animal Kunitz-type proteinase inhibitor homoly

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Lissue factor pathway inhibitor precursor - rhesus macaque
N;Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation inhib
C;Species: Macaca mulatta (rhesus macaque)
C;Dates: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JC2264
R;Kamei, S.; Kamikubo, Y.; Hamuro, T.; Fujimoto, H.; Ishihara, M.; Yonemura, H.; Miyamot
J. Blochem. 115, 708-714, 1994
A;Filtle: Amino acid sequence and inhibitory activity of rhesus monkey tissue factor path
A;Reference number: JC2264; MUID:94375417; PMID:8089087
A;Accession: JC2264; MUID:94375417; PMID:8089087
A;Cross-references: UNIPROT:Q28864; UNIPARC:UPI0000136C90; GB:S73337; NID:9685016; PIDN:
A;Experimental source: liver
C;Comment: This protein inhibite the activities of factor Xa and tissue factor-factor VI
C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
F;29-304/Product: tissue factor pathway inhibitor homology <BP1>
F;3217-267/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;3217-267/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;217-267/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>
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F;39-304/Product: tissue factor pathway inhibitor #status experimental <MAT>
F;284-104/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;125-175/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;125-175/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;284-289/Region: heparin binding #status predicted
F;30/Binding site: phosphate (Ser) (covalent) #status experimental
F;54-104,63-87,79-100,125-175,134-158,150-171,217-267,226-250,242-263/Disulfide bonds:
F;54-104,63-87,79-100,125-175,134-158,150-171,217-267,226-250,242-263/Disulfide bonds:
F;64/Inhibitory site: Lys (cosqulation factor VII/tissus factor complex) #status experimental
F;145,195,256/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;227/Inhibitory site: Arg (unidentified proteinase) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 2q32-2q32
A; Introns: 41/1; 107/1; 1
C; Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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F;54-104,63-87,79-100,125-175,134-158,150-171,217-267,226-250,242-263/Disulfide bonds: #E F;64/Inhibitory site: Lys (coagulation factor VII/Eissue factor complex) #status predicte F;135/Inhibitory site: Arg (coagulation factor X) #status predicted F;135/Inhibitory site: Carbohydrate (Asn) (covalent) #status predicted F;145,195;256/Binding site: carbohydrate (Asn) (covalent) #status predicted F;227/Inhibitory site: Arg (unidentified proteinase) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue factor pathway inhibitor precursor - rat
N,Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coag
C,Species: Rattus norvegicus (Norway rat)
C,Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C,Accession: X02213
R,ERDJYOJ1, K.; Emi, M.; Mukai, T.; Kato, H.
J. Biochem. 111, 681-687, 1992
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A, Title: cDNA cloning and expression of rat tissue factor pathway inhibitor (TFPI).
A, Reference number: JX0213; MUID:92348361; PMID:1639767
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Best Local S
Matches 91
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Best Local S
Matches 84
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 53 CAMKAEDGPCKAMIRSYYFNMNSHQCEEFIYGGCRGNKNRFDTLEECRKTCIPGYKKTTI
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                                    CLLPLDYGPCRALLLRYYYDRYTQSCRQFLYGGCEGNANNFYTWEACDDAC-----
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                                                                                      28.8%; Score 376; DB 1
33.1%; Pred. No. 2e-26;
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                                                                                                         Length 302;
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---WRIEKVPKVCRLQVSVDDQ--CEGSTEKYFFNLSSMTCEKFFSGGCHRNRIENRFPD 141

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A;Crober reference; warrance a; (Cabb, J.W.; Buonassis), V.

R;Colburn, P.; Crabb, J.W.; Buonassis), V.

J. Cell. Physiol. 148, 320-326, 1991

A;Title: Enhanced inhibition of tissue factor by the extended form of an endothelial cell a;Title: Enhanced inhibition of tissue factor by the extended form of an endothelial cell a;Title: Enhanced inhibition of tissue factor pathway inhibitor; animal Kunitz-type protein a;Cross-references: UNIPARC:UPIO001762A6

A;Cross-references: UNIPARC:UPIO001762A6

C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor homology <BP1>
F;50-100/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;121-171/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>
F;213-263/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>
                    RESULT 7
853325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-300 <WESS>
A;Cross-references: UNIPARC:UPI000016C583;
R;Colburn, P.; Crabb, J.W.; Buonassisi, V.
J. Cell. Physiol. 148, 320-326, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lipoprotein-associated coagulation inhibitor precursor - rabbit N;Alternate names: endothelial cell coagulation inhibitor; endothelial cell tissue C;Species: Oryctolagus cuniculus (domestic rabbit)
G;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999 C;Accession: S12143; A63373
R;Wesselschmidt, R.L.; Girard, T.J.; Broze Jr., G.J.
Nucleic Acids Res. 18, 6440, 1990
A;Title: CDNA sequence of rabbit lipoprotein-associated coagulation inhibitor.
A;Reference number: S12143; MUID:91057146; PMID:2136251
A;Accession: S12143
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  factor
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                                                                                                                                                                                                                                                                                                                                                                                                           RYTQSCRQFLYGGCEGNANNFYTWEACDDACWR------
pathway
                                                                                                                                                                                                                                                                                                                                                                           ILAHOCEEFIYGGCEGNENRFESLEECKEKCARDYPKMTTKLTFOKGKPDFCFLEEDPGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLLFLTEAALGDAAQ8------PTGNNABICLLPLDYGPCRALLLRYYYD
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                                                                                                                                                     CDAFTYTGCGGNDNNFVSREDCKRACAKAL------KKKKKMP 219
                                                                                                                                                                                                 FQVDDHRTQLNTVNNTLINQPTKAPRRWAFHGPYWCLPPAERGLCQANBIRFFYNAIIGK
                                                                                                                                                                                                                                                                                        CR-----GYITRYFYNNQSKQCERFKYGGCLGNL--NNFESLEECKNTCENPTSD
                                                                                                                                                                                                                                                                                                                                  CRLQVSVDDQCEGSTEKYFFNLSSMTCEKFFSGGCHRNRIENRFPDEATCMGFC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLLGLVPAPVSSAAEEDEEFTNITDIKPPLQKPTHS---FCAMKVDDGPCRAYIKRFFFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEGLCSANVTRYYFNPRYRTCDAFTYTGCGGNDNNFVSREDCKRACAK-ALKKKKKMPKL
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                                                                                                            CRPFKYSGCGGNENNFTSKKACITACKKGFIPKSIKGGLIKTKRKKKKQP 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
  inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.5%; Score 372.5; DB 2; 29.7%; Pred. No. 4.2e-26;
                                                                                                                                                                                                                                             -----APKKI----PSFCYSPKDBGLCSANVTRYYFNPRYRT
  rabbit
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                                                                                                                                                                                                                                                                                                                                                                                                                     -----IEKVPKV
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hypothetical protein W01F3.3 - Caenorhabditis elegans C;Spectes: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct-1999 #tcC;Accession: T26063
                                                                                                                                                A; Cross-references: UNIPROT:045881; A; Experimental source: clone W01F3
                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-2225 <WIL>
                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, A; Reference number: Z20145
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C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 17-Mar-2003
C;Accession: S53325
C;Accession: S53325
R;Girard, T.J.; Gailani, D.; Broze Jr., G.J.
Biochem. J. 303, 923-928, 1994
                                                              A; Introns:
                                                                               A; Map position:
                                                                                                     A;Gene: CESP:W01F3.3
                                                                                                                                                                                                                           A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                               R; Cummings,
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A;Molecule type: mRNA
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Matches 92
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                     Query Match
  Local
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Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCRQFLYGGCEGNANNFYTWEACDDACWRI------EKV----PKVCRLQVSVDDQ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLQHDSESGGLQHDSESGGLQHDSGDNTSPPVSVNNDSFTPRPPTVSSPLEFYGPSWCLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRGFVTRYYYNNVSSKCEGFKYGGCLGNL--NNFETLEQCKNTCEGSIDLLMDETVNNTG
                                                              56/1;
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                                                                                                                                                                                                                                                                                                                                               #sequence_revision 15-Oct-1999 #text_change
                                                          100/1; 142/3; 271/3; 451/1; 525/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.5%; Score 346.5;
24.6%; Pred. No. 1.26
rative 35; Mismatches
23.4%;
Score 305.5;
Pred. No. 3.1
                                                                                                                                                                                                                                                                                           March
                                                                                                                                                                   UNIPARC: UPI00000816EC; EMBL: 292815;
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.5; DB 2;
3.1e-19;
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.es 88;
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                     Length 2225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 159;
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                                                            774/1; 1093/1;
                                                                                                                                                                                                                                                                                                                                                        09-Jul-2004
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                                                                                                                                                                   PIDN: CAB07294.1;
                                                            1178/1;
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hypothetical protein C37C3.6b - Caenorhabditis elegans C,8pecles: Caenorhabditis elegans C,8pecles: Caenorhabditis elegans C,Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change C,Accession: T34395, T34394
R,Geisel, C., Bradshaw, H.
submitted to the EMBL Data Library, July 1996
A,Description: The sequence of C. elegans cosmid C37C3.
A,Reference number: Z21518
A,Accession: T34395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-2167 <GEI>
A;Crose-references: UNIPROT:076840; UNIPARC:UPI000007D957;
A;Experimental source: strain Bristol N2; clone C37C3
A;Accession: T34394
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary;
                                                                                       RESULT 10
T33216
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A;Residues: 1-1555;'SKF' <GE2>
A;Residues: 1-1555;'SKF' <GE2>
A;Crose-references: UNIPARC:UPI000085C9F; EMBL:U64857; PIDN:AAC25867.1; GSPDB:GN00023;
A;Experimental source: strain Bristol N2; clone C37C3
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hypothetical protein T07H8.4 - Caenorhabditis elegans C;Bpecies: Caenorhabditis elegans C;Bpecies: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Accession: T33216
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A;Introns: 32/3; 104/2; 156/2; 207/1; 459/2; 536/3; 577/2; 1105/3; 1367/1; 1438/1;
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Best Local 8
Matches 64
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;Map position: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FATMQECRSRCVMAMKKSPVATCEADIEVGECAGVPSRFAFDKSINACRSFTYGGCGGNA 943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGALPELCMLPEQRGSCYDNILRWREDSEKSQCYTEMYSGCNPNANHETSQETCERACGK
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                                                                                                                                                                                     OOSCRPGDTKSEDICTLR
                                                                                                                                                                                                                                KRACAKALKKKKKKMPKLR
                                                                                                                                                                                                                                                                              CRVETLWSNNTDFCTLERSAGFCTDSISMWYFDSTHLDCKFFTYGGCRGNQNRFVSKEQC
                                                                                                                                                                                                                                                                                                       CAPKKIPS----FCYSPKDEGLCSANVTRYYFNPRYRTCDAPTYTGCGGNDNNFVSREDC
                                                                                                                                                                                                                                                                                                                                                                                                                      IEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSMTCEKFFSGGCHRNRIENRFPDEATCMGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.2%; Score 303; DB 2; Length 2167; larity 32.3%; Pred. No. 5.1e-19; Conservative 35; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208
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RESULT 11
C89114
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A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1558 <STO>
A;Residues: 1-1558 <STO>
A;Cross-references: UNIPROT:Q81710; UNIPARC:UPI0000085C9F; GB:chr_V; PIDN:AAC25867.1;
C;Genetics: C37C3.6a
A;Map position: 5
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A;Residues: 1-1965 <GAT>
A;Cross-references: UNIPARC:UPI000017BB7E; EMBL:AF067945; PIDN:AAC17681.1; GSPDB:GN00023;
A;Experimental source: strain Bristol N2; clone T07H8
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submitted to the RMBL Data Library, May 1998
A;Description: The sequence of C. elegans cosmid T07H8.
A;Reference number: Z21303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Note: genome: A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein C37C3.6a [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: C89114
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Best Local Similarity
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                                          94 KVCRLQV-----SVDDQ-----CEGSTEKYFFNLSSMTCEKFFSGGCHRNRIENRFP 140
                                                                                                                                              34 BICLLPLDYGPCRALLLRYYYDRYTOSCROPLYGGCEGNANNFYTWBACDDACWRIBKVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCGGNRNRFATQDICENTCNGLMNSNDPRICSFSPDWGSCNQLRYVWFYNLTRGTCDQFL 1762
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                                                                                                 DACHLNVDQGRCKGAFDSWYYEVATGSCVTFKYTGCGGNANRFASKDQCESLC--VKPAS
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EAASAGIDGAAGINSVCDEAKDTGPCTNFVTKWYYNKADGTCNRFHYGGCQGT--NNRFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHYTGCGKSGNNFLTKEECQTKCEKRFPRAAPSKKKAKLK 1859
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30.0%; Pred. No. 1.1e-18;
ative 24; Mismatches 80;
                                                                                                                                                                                              22.4%; Score 292.5; DB 2; 33.0%; Pred. No. 3.2e-18; tive 26; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GSTEK----YFFNLSSMTCEKFF
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R; anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998
A; Title: Genome sequence of the nematode C. elegans: a platform for investigating: A; Note: See websites genome.wustl.edu/gsc/C elegans/ and www sanger.ac.uk/Projects A; Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 199 A; Accession: H88380
A; Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 199 A; Accession: H89380
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1522 <STO>
A; Cross-references: UNIPARC:UPI000017A5B5; GB:chr_III; PIDN:AAA20672.1; PID:g52971.
A; Note: highly similar to ZC84.1
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, June 1996
A;Reference number: Z19762
A;Reference number: Z19762
A;Reference number: Z19763
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-922 <WIL>
A;Residues: 1-922 <WIL>
A;Cross-references: UNIPROT:Q21418; UNIPARC:UPI00000762C2; EMBL:Z75545; PIDN:CAA99886.1;
A;Genetides:
A;Genetides:
A;Genetides: CESP:K10D3.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein T22F7.3 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: H88380
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R;McMurray, A.
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A; Introns: 60/1; 228/1;
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RESULT 14
E88550
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A;Cross-references: UNIPROT:Q03610; UNIPARC:UPI000013BAA7; GB:chr_III; PIDN:CAA79569.1;
A;Note: similar to Serine protease inhibitor, Kunitz type
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A;Title: Genome sequence of the nematode C. elegan
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C;Specises: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: E88550
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A; Map position:
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                                                                                                                                                                                                                                                                61 CROFLYGGCEGNANNFYTWEACDDACWRIEKVPK-----
                                                                                                                                                                                                                                                                                                                                     74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 PTGNNAEICLLPLDYGPCRALLLRYYYDRYTQSCRQFLYGGCEGNANNFYTWEACDDACW
                                                                                                                                                                                                                                                                                                                                                                                            Similarity
RCCPTRAYMCGLPPQQGTQCGANYVQRYYFNIVTSQCTSFQFGGCDGNANNFLNIQQCRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                    ENRFPDEATCMGFCAPKKIPS----
                                                                             SNNFANRDACESYCSVGGCPNGGTPLRDHSGMVMVCGAQQTSCPDSHECIPVLVGNSLIN
                                                                                                                                                    YECYFDGSQWGCCPTKAFTCSLNTDSGIQCGAGSTFKYYYNPQTQNCBSPQYNGCDGN--
                                                                                                                                                                                                                            CQMFEYTGCQGNDNNFDSIMDCQNFCKNAIPEPKCIQGQAYKDMFGNFVTCSNGMGCPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKGVQCGSGRSYRYYFNSNKQSCBSFQYBGCDGN--ANNFLTSEDCQHYCGVGGCPNGGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GIHVEPKCQHGRAFRDRNGNFQQCSDKQNGPKCPVNYVCSFDGTTHGCCPTKAFTCSLNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIBKVPK-----
                                                                                                                                                                                      ------VCRLQVSVDDQC-EGSTEKYFFNLSSMTCEKFFSGGCHRNRI 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTRYYFNPRYRTCDAFTYTGCGGNDNNFVSREDCKRACAKA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVDDQC-EGSTEKYFFNLSSMTCEKFFSGGCHRNRIENRFPDEATCMGFCA------
                                           -----FCYSPKDEGL-CSAN-VTRYYFNPRYRTCDAFTYTGCGGNDNNFVSREDCKR 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLRDEATNKPMSCSEQKSCPSTHECLTIPVNGHVGSRCCPTKQHICSQPPQQGNHCSKIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----FCYSPKDEG-LCS-AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGRFYFNIVTRECATFOYNGCNGNLNNFATOSECNNFCSSA 803
                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                          20.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.4%; Score 279.5; DB 2
26.0%; Pred. No. 4.7e-17;
Live 21; Mismatches 86
                                                                                                                                                                                                                                                                                                                                                                         25;
                                                                                                                                                                                                                                                                                                                                                                                        Score 271.5; DB 2;
Pred. No. 2.3e-16;
                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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98
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R;Thomas, K.
submitted to the EMBL Data Library, December 1992
A;Reference number: $28285
A;Recession: $28291
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2844 <THO>
A;Cross-references: UNIPROT:Q03610; UNIPARC:UPI000017BCE9; EMBL:Z19157
A;Cross-references: UNIPROT:Q03610; UNIPARC:UPI000017BCE9; EMBL:Z19157
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P;220-274/Domain: animal Kunitz-type proteinase inhibitor homology <BPI1>P;230-274/Domain: animal Kunitz-type proteinase inhibitor homology <BPI2>P;443-395/Domain: animal Kunitz-type proteinase inhibitor homology <BPI3>P;442-492/Domain: animal Kunitz-type proteinase inhibitor homology <BPI3>P;442-492/Domain: animal Kunitz-type proteinase inhibitor homology <BPI3>P;546-598/Domain: animal Kunitz-type proteinase inhibitor homology <BPI5>P;1662-1716/Domain: animal Kunitz-type proteinase inhibitor homology <BPI6>P;1797-1839/Domain: animal Kunitz-type proteinase inhibitor homology <BPI9>P;1845-1895/Domain: animal Kunitz-type proteinase inhibitor homology <BPI9>P;1952-2004/Domain: animal Kunitz-type proteinase inhibi
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C;Species: Caenorhabditis elegans
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: 828291
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Search completed: March 9, 2006, 19:57:33 Job time : 42 secs
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                                                                                                                                                                                                                                                        207 AC 208
                                                                                                                                                                                                                                                                                                                                           645 RCCPTRAYMCGLPPQQGTQCGANYVQRYYENIVTSQCTSFQPGGCDGNANNFLNIQQCRN 704
                                                                                                                                                                                                                                                                                                                                                                                                                                       157 -----FCYSPKDEGL-CSAN-VTRYYFNPRYRTCDAFTYTGCGGNDNNFVSREDCKR 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             527 YECYFDGSQWGCCFTKAFTCSLNTDSGIQCGAGSTFKYYYNPQTQNCESFQYNGCDGN-- 584
                                                                                                                                                                          705 PC 706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 ENRFPDEATCMGFCAPKKIPS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25; Mismatches 86; Indels 117; Gaps
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Maximum Match 100%
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               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: uniprot_sprot:*
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databases. 6/S0167-4781(00)002 ., Kisiel W.; he human tissue fac he human tissue fac grape J.G., Derge J.G., Derge J.G., Schuler G. fer C.F., Bhat N.K. Wang J., Heieh F., n G.M., Hong L., vant T.L., Scheetz	ENCE. B., Hirahara F., proteinase inhibit lacental protein 5 lacental protein 5 lacental protein 5	(TPPI-2) (Placental tebrata, Euteleostomi; tes; Catarrhini; Hominidae	099qr0 dros 045881 caer 045887 caer 08mpv5 caer 0500t97 caer 05zr35 caer 05zr36 caer 05zr39 caer 05zr39 caer 05zr40 caer 05zr40 caer 05zr40 caer 05dwp1 caer 081710 caer
98-0; D.,	or	; nidae;	drosophila caenorhabdi

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R MIM; 600033; -.

R GO; GO:0005578; C:extracellular matrix (sensu Metazoa); TAS.

R GO; GO:0005201; F:extracellular matrix structural constituent; TAS.

R FINERO; IPRO0220; Prot_inh_Kunz-m.

R PIAM; PIRO01620; TFPI; 3.

R PIAM; PIRO1059; BASICPTASE.

R PROSITE; PS00202; Prot_Inh_Kunz-m; 3.

R PROSITE; PS00200; BPTI_KUNITZ_1; 3.

R PROSITE; PS00219; BPTI_KUNITZ_2; 3.
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A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
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A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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A Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
B Bufterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
A Generation and initial analysis of more than 15,000 full-length human
A Think T. Schmutz M. A.,
A Parc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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EMBL; L27624; AAA20094.1; -; mRNA.

EMBL; AC002076; AAS02022.1; -; Genomic_DNA.

EMBL; AF217542; AAX13254.1; -; Genomic_DNA.

EMBL; BC005330; AAH05330.1; -; mRNA.

PIR; A54951; A54951.

HSSP; P10646; IIRH.

Ensembl; ENSG0000105825; Homo sapiens.

HGNC; HGNC; 11761; TFPIZ.
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Biochem. Biophys. Res. Commun. 151:630-631(1988).

-I- FUNCTION: Seems to inhibit trypsin, factor VIIa/tissue factor, weakly factor Xa. Has no effect on thrombin.

-I- SUBCELLUIAR LOCATION: Secreted.

-I- TISSUB SPECIFICITY: Umbilical vein endothelial cells, liver, placenta, heart, pancreas, and maternal serum at advanced
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Buetzow R., Huhtala M.-L., Bohn H., Virtanen I.,
"Purification and characterization of placental particles."
Biochem. Biophys. Res. Commun. 150:483-490(1988).
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DOMAIN: This inhibitor contains three inhibitory domains.

SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
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Submitted (UUL-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
EMBL; AY691946; AAU04568.1; -; mRNA.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:000467; F:serine-type endopeptidase inhibitor activity;
GO; GO:0004867; F:serine-type endopeptidase inhibitor activity;
GO; GO:0007596; P:blood coagulation; IEA.
GO; GO:0007596; P:blood coagulation; IEA.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Tissue factor pathway inhibitor 2.
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CROFLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSM
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Pred. No. 5.4e-111;
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975ABA5C53F7C65F
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                                                                            3.4e-111;
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RX PUNMed=14702039; DOI=10.1038/ngl285;

RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Simura K., Makita H.,

RA Yamamoto J.-I., Saito K., Kawai T., Ishibahara T., Tanaka T., Ishii S.,

RA Yamamoto J.-I., Saito K., Kawai T., Iswayanagi T., Wagatsuma M.,

RA Yamamoto J.-I., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,

RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,

RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Puruya T., Kikawa E.,

RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Puruya T., Kikawa K.,

RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,

RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,

RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,

RA Nomura Y., Abe K., Kamita M., Watanabe M., Hiraoka S., Chiba Y.,

RA Ishida S., Ono Y., Takiguchi S., Watanabe M., Hara H., Tanase T.-O.,

RA Nomura Y., Togiya S., Komai P., Hara R., Takeuchi K., Arita M.,

RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,

RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,

RA Yoshikawa S., Genoh A., Mizoguchi H., Goto Y., Shimizu P., Wakebe H.,

RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,

RA Yamazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,

RA Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Pujiwara T.,

RA Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Pujiwara T.,

RA Notitani R., Kawakami T., Noguchi S., Itoh T., Shigatu P., Wakebe H.,

RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,

RA Mishiga Sugawa S., Satoh T., Sinizo M., Sasaki M.,

RA Mishiga S., Makajima Y., Mizuno T., Morinaga M., Sasaki M.,

RA Mishiga S., Makajima Y., Mizuno T., Masaho Y., Nakagawa K.,

RA Nakaga S., Nakajima Y., Mizuno T., Masaho Y., Nakagawa K.,

RA Nakaga S., Nakagiwa T., Satoh T., Sugano S.,

RA Nakaga S., Satoh T., Sugano S.,

RA Nakaga S., Satoh
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QBNAK6 HUMAN
QBNAK6;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein FL/35180.
Homo sapiens (Human)
                                                                                                                                                                                                                                  PRINTS; PR00759; BASICPTASE.
ProDom; PD000222; Prot_Inh_Kunz-m;
                                                                                                 InterPro; IPR002223; Prot_inh_Kunz-m.
InterPro; IPR008296; Prot_inh_TPPI.
Pfam; PP00014; Kuntlz_BPTT; 3.
PIRSP; PIRSP001620; TFPI; 1.
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    iP; P10646; IIRH.
    GO:0005576; C:extracellular region; IEA.
    GO:0030414; F:protease inhibitor activity;
    GO:0004867; F:serine-type endopeptidase inh
    GO:0007596; P:blood cosgulation; IEA.

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SEQUENCE
                                                                                                                                                                                                      PROSITE; PS00280; BPTI KUNITZ 1; 1.
PROSITE; PS50279; BPTI KUNITZ 2; 2.
NON TER 1 1
SEQUENCE 167 AA; 19365 MW; 16C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 23, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to tissue factor pathway inhibitor 2 (Fragment).
                                                                                                                                                                                                                                                           ProDom; PD000222; P; SMART; SM00131; KU;
                                                                                                                                                                                                                                                                                   GO; GO:0004867; P:serine-type endopeptidase InterPro; IPR002223; Prot inh Kunz-m. Pfam; PF00014; Kunitz BPTI; 3. PRINTS; PR00759; BASICPTASE.
                                                                                                                                                                                                                                                                                                                                        Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

-- SIMILARITY: Contains 2 BPTL/Runitz inhibitor domains.

EMBL, BC034155, AAH34155.1; -; mRNA.

HSSP; P10646; 1IRH.
                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (JUL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8NE89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOMO.
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HUMAN
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                        189
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 121
                                                                                                                                                     al Similarity
167; Conserv
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PS50279; BPTI_KUNITZ_2; 3.
224 AA; 25795 MW; F586
                                                                GCHRNRIENRFPDBATCMGFCAPKKIPSFCYSPKDEGLCSANVTRYYFNPRYRTCDAFTY
                                                                                                                  CEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSMTCEKFFSG
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                                                                                                    CEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSMTCEKFFSG
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                         TGCGGNDNNFVSREDCKRACAKALKKKKKMPKLRFASRIRKIRKKQF 235
                                                  GCHRNRIENRFPDEATCMGFCAPKKIPSFCYSI
                                                                                                                                                                                                         167 AA; 19365 MW; 16C204E96071F27D CRC64;
                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                      Prot_Inh_Kunz-m;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                  72.2%; Score 943; I
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Pred. No. 3.3e
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RESULT 5
QYYRQ8 BOVIN PRELIMINARY;
AC QYYRQ8;
DT 01-OCT-2003 (TrEMBLrel. 25,
DT 01-OCT-2003 (TrEMBLrel. 25,
DT 01-OCT-2003 (TrEMBLrel. 26,
DT 01-MAR-2004 (TREMBLrel. 26,
DT 01-MAR-2004 (TREMBLrel. 26,
DT 01-MAR-2004 (TREMBLrel. 26,
DE Tissue factor pathway inhib:
OS Bos taurus (Bovinae).
OC Eukaryota; Metazoa; Chordat;
OC Mammalia; Eutheria; Laurasii,
OC Pocora; Bovidae; Bovinae; B
OX NCBI TaxID-9913;
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE-22802738; PubMed-12
RA NUCLEOTIDE SEQUENCE.
RX MEDLINE-22802738; PubMed-12
RA NUCLEOTIDE SEQUENCE.
RY MOLECULAR Cloning, express
factor pathway inhibitor-2.
RL Arch. Biochem. Biophys. 417
RN [2]
RP NUCLEOTIDE SEQUENCE.
RL Arch. Biochem. Biophys. 417
RN [2]
RR HSCOTT PROMOSE (FEB-2003) to the
CC -1- SIMILARITY: Contains 3
DR EMBL; AY23486; ANO84035.1;
DR HSSP; P00981; IDTK.
DR GO; GO:0007596; P:Berine-ty
DR GO; GO:0007596; P:Broct-in-ty
GO; GO:00014867; P:Berine-ty
GO; GO:00014867; P:Berine-ty
GO; GO:00014; Kunitz BPTI;
DR PINSF; PHRSP001529; BASICPTASE
DR PINSF; PHRSP001529; PTOT-In-
DR PINSF; PHRSP001529; BASICPTASE
DR PROSITE; PS00279; BPTI KUNI
DR PROSITE; PS00279; BPTI KUNI
SQ SEQUENCE 234 AA; 26675 M
  RESULT
QBCF99
ID QB
AC QB
AC QB
DT QI
DT 01
DT 01
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Best Local Similarity
Matches 171; Conserv
LT 6
99 RAT
908CF99; RAT PRELIMINARY; PRT; 230 AA.
08CF99;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Tissue factor pathway inhibitor-2 precursor.
Name=tfpi-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P00981; IDTK.

GO; GO:000576; C:extracellular region; IEA.

GO; GO:000576; C:extracellular region; IEA.

GO; GO:00030414; F:protease inhibitor activity; IEA.

GO; GO:0004867; F:serine-type endopeptidase inhibitor activity;

GO; GO:0007596; P:blood coagulation; IEA.

InterPro; IPR00223; Prot_inh Kunz-m.

InterPro; IPR00223; Prot_inh TPPI.

Pfam; PP00014; Kunitz_BPTI; 3.

PIRSP; PIRSP001620; TPPI; 1.

PRINTS; PR00759; BASICPTASE.

PRODOM; PD00022; Prot_Inh_Kunz-m; 3.

PROSCOSO. BASICPTASE.

PRODOM; PD00022; Prot_Inh_Kunz-m; 3.

PROSCOSO. BRSICPTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22802738; PubMed=12921785; DOI=10.1016/S0003-9861(03)00332-1; DU X., Deng F.M., Chand H.S., Kisiel W.; "Molecular cloning, expression, and characterization of bovine tissue factor pathway inhibitor-2."; Arch. Biochem. Biophys. 417:96-104(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence up
01-MAR-2004 (TrEMBLrel. 26, Last annotation
Tissue factor pathway inhibitor-2.
Bob taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00280; BPTI_KUNITZ_1; 3.
PROSITE; PS50279; BPTI_KUNITZ_2; 3.
SEQUENCE 234 AA; 26675 MW; 401E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deng F.-M., Kisiel W., Sun T.-T., Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains
EMBL; AY234861; AAO84035.1; -; mRNA.
                                                                                                                                                                                                                                                                               178
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                                                                                                                                                                                                                                                                                                 RTCDAFTYTGCGGNDNNFVSRBDCKRACAKALKKK--KKMPKLRFASRIRKIRKKQF 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRQFLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MDPARPLGLSILLLELTEAALGDAAQBPTGNNABICLLPLDYGPCRALLLRYYYDRYTQS
                                                                                                                                                                                                                                                                          KACEAFNYTGCGGNDNNFVNLKDCKRTCVKALKKEKNKKMPRLLLANRRLKIKKKOF
                                                                                                                                                                                                                                                                                                                                                                        TCKKFISGSCHSN--ENRFPDEATCMDFCAPKRAPVFCYSPKDEGLCSANVTRYYFNPRH
                                                                                                                                                                                                                                                                                                                                                                                                      TCEKFFSGGCHRNRIENRPPDEATCMGFCAPKKIPSFCYSPKDEGLCSANVTRYYFNPRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CREFMYGGCEGNANNFETLEACNEACWKIEKVPKICKLKVN-KKOCGELREQYFFNLSSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MDSVRPLWLMLLSLLLVGTALGDASQAPPGNNAEICLLPPDDGPCRARIPSYYYDRYTQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 939.5; |
Pred. No. 1.5e
23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    401EEC84D589B422 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234
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\.5e-77;
зя
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RESULT TREAL TREAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Sim
Matches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGD; 628629; Tfpi2.

GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0004867; F:serine-type endopeptidase inl
GO; GO:0004867; F:serine-type endopeptidase inl
GO; GO:0007596; P:blood coagulation; IEA.

InterPro; IPR002223; Prot_inh_Kunz-m.
InterPro; IPR008296; Prot_inh_TFPI.

Pfam; PF00014; Kunitz BPTI; 3.

PIRSF; PIRSF001620; TFPI; 1.

PIRSF; PRSF001620; TFPI; 1.

PRINTS; PR00759; BASICPTASE.

PRODOM; PD000222; Prot_Inh_Kunz-m; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Sprague Dawley; TISUE=Placenta; MEDLINE=22183372; PubMed=12195712; Hisaka T., Kisiel W., Rosenbaum J.; "cDNA cloning and tissue distribution of factor pathway inhibitor-2."; Thromb. Haemost. 88:356-357(2002).

-! SIMILARITY: Contains 3 BPTI/Kunitz in EMBL; AJ428954; CAD22046.1; -; mENA. HSSP; P10666; 11RH.
                                                        Bukaryota; Metazoa; C
Mammalia; Butheria; E
Muroidea; Muridae; Mu
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Tissue factor pathway inhibitor 2 precursor (
                                                                                                                                                                                                                                                                                                                                                                                                                                             035536;
                                                                                                                                                                                                                    Name=Tfp12;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPP12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50280; BPTI_KUNITZ_1; PROSITE; PS50279; BPTI_KUNITZ_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ensemb1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Bubheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRQFLYGGCEGNANNFYTWEACDDACWRIEKVFKVCRLQVSVDDQCEGSTEKYFFNLSSM
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25
230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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230
                                                                                                                                        Euarchontoglires;
                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.1%;
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; Score 654; DB 2;
; Pred. No. 1.7e-51;
25; Mismatches 74

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tissue factor pathway inhibitor-2.
; 07CCD5B9F7D43ED9 CRC64;
                                                                                                                                                                                                                                                                                            precursor (TFPI-2).
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ptidase inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   230
                                                                                                                                                Glires; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ortholog
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                                                                                                                                                Sciurognathi;
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SEQUENCE

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RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA).

RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA).

RC STRAIN=C57BL/6J TISSUE-Mammary gland;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

RX Altechul S.F., Zeeberg B., Buctow K.H., Scheefer C.F., Bhat N.K.,

RX Altechul S.F., Zeeberg B., Buctow K.H., Scheefer C.F., Bhat N.K.,

RX Altechul S.F., Zeeberg B., Buctow K.H., Scheefer C.F., Bhat N.K.,

RX Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RX Stapleton M., Soares M.B., Bonaldo M.F., Rubin G.M., Hong L.,

RX Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RX Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RX Stapleton M., Goulanne F.J., Male S., Carninci P., Prange C.,

RX Raha S.S., Loquellano N.A., Peters G.J., Moramson R.D., Mullahy S.J.,

RX Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunarathe P.H.,

RX Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RX Raha S.S., Helton B., Kettenan M., Madan A., Rodrigues S., Sanchez A.,

RX Raha S., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RX Rodriguez A.C., Grimwood J., Schmutz J., Myzrs R.M.,

RX Rodriguez A.C., Grimwood J., Schmutz J., Myzrs R.M.,

RX Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human

"Generation and initial analysis of more than 15,000 full-length human
              PRINTS; PRO0759; BASICPTASE.

ProDoms, PD000222; Prot_Inh_Kunz-m; 3.

SMART; SMO0131; KU; 3.

PROSITE; PS00280; BPTI_KUNITZ_1; 2.

PROSITE; PS00279; BPTI_KUNITZ_2; 3.

Blood_coagulation; GlycoproteIn; Protease inhibitor; Serine protease inhibitor; Signal.

Serine protease inhibitor; Signal.

Serine protease inhibitor; Signal.

Serine protease inhibitor; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D50586; BAA22585.1; -; mRNA.
EMBL; AF180353; AAF40412.1; -; Gen
EMBL; BC021639; AAH21639.1; -; mRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20132652; PubMed=10669168;
Kazama Y., Kamei S., Kuijper J.L., Foster D.C., Kisiel W.;
"Nucleotide sequence of the gene encoding murine tissue factor pathway inhibitor-2.";
                                                                                                                                                                                                       MGI: MGI: 108543; TÉPI2.

GO; GO:0005615; C:extracellular space; TAS.
InterPro; IPR002223; Prot inh Kunz-m.
InterPro; IPR008296; Prot inh TPPI.
Pfam; PP00014; Kunitz BPTI; 3.

PIRSP; PIRSP001620; TFPI; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
FUNCTION: Seems to inhibit trypsin, factor VIIa/tissue factor,
weakly factor Xa. Has no effect on thrombin.
SUBCELLULAR LOCATION: Secreted.
TISSUB SPECIFICITY: Highly expressed in placenta. Also expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B Swiss-Prot entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN: This inhibitor contains three inhibitory domains. SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in liver and kidney.

DOMAIN: This inhibitor
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                                                                                                                                                                                                                                                                                                                                                 .; ENSMUSG00000029664; Mus musculus.
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By similarity.
Tissue factor
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pathway inhibitor 2
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RX MEDLINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RX Klausner R.D., Collins F.S., Wagner L., Shenefer C.F., Bhat N.K.,
RX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RX Hopkins R.F., Jordan B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RX Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RX Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RX Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RX Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RX Rahas S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RX Rahards S., Worley K.C., Hale S., Garcia A.M., Gy L.J., Hulyk S.W.,
RX Rahay J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RX Rahay J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RX Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RX Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RX Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RX Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
MGC68843 protein.
Xenopus lasvis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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/5 XENLA
Q7TOZ5_XENLA PRELIMINARY;
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BPTI/Kunitz inhibitor 2.
BPTI/Kunitz inhibitor 3.
BPTI/Kunitz inhibitor 3.
Reactive bond (By similarity).
Reactive bond (By similarity).
Reactive bond (By similarity).
N-linked (GlcNAc. . .) (Potenti
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Matches 107;
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QSFVY6;
10-MAY-2005 (TrEMBLrel. 30,
10-MAY-2005 (TrEMBLrel. 30,
10-MAY-2005 (TrEMBLrel. 30,
                                                               Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
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NUCLEOTIDE SEQUENCE
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GG; GO:0005414; F:protease inhibitor activity;
GO; GO:0004867; F:serine-type endopeptidase inh
GO; GO:0007596; P:blood coagulation; IEA.
InterPro; IPR002223; Prot inh Kunz-m.
InterPro; IPR002223; Prot inh Kunz-m.
InterPro; IPR00223; Prot inh TFPI.
Pfam; PP00014; Kunitz_BPII; 3.
PIRSP; PIRSP001620; TFPI; 1.
                                           NCBI_TaxID=8364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00759; BASICPTASE.
ProDom; PD000222; Prot_Inh_Kunz-m;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klein S., Strausberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
-I- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
EMBL; BC055972; AAH55972.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00280; BPTI_KUNITZ_1; 3.
PROSITE; PS50279; BPTI_KUNITZ_2; 3.
SEQUENCE 224 AA; 25538 MW; 11C2D1C4C789445B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
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VCKKGTKRPRNQNPKIPRIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PMQGNTTVCLLFLDEGPCKALIFHYYXDRYTQTCQEFFYGGCDGNANNFVSMEDCEKPCW
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Last sequence update)
Last annotation updat
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Pred. No. 9e-50;
5; Mismatches
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RESULT 10
Q4RDL7_TET
ID Q4RDL
AC Q4RDL
DT 13-SE
DT 13-SE
DT 13-SE
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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA RA Brownstein M.J., Wedin R.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

RA Rahes S.S., Loquellano N.A., Peters G.J., Abramaon R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Whiting M., Madan A., Young A. C., Shevchenko Y., Bouffard G.G.,

RA Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Radriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length human

"Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RA Klein S., Gerhard D.S.;

RA Klein S., Gerhard D.S.;

RA Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.

CC --- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.

CC EMBL; BC089705; AAH89705.1; --; mRNA.

RA GO; GO:0005576; C:extracellular region, IEA.

RO; GO:0030414; F:protease inhibitor activity; IEA.

RO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.

CO; GO:0007596; P:blood coagulation; IEA.

R GO; GO:0007596; P:blood coagulation; IEA.

R GO; GO:0007596; P:blood coagulation; IEA.

R GO; GO:0007596; P:blood coagulation; IEA.

R FINTERPO; IFR002223; Prot_inh_TRDI.

PEAM; PROSO14; Kunitz BPTI; 3.

R PIASF; PIRSPO01620; TFPI; 1

R PRINTS; PRO0759; BASICPTASE.

RR PROSITE; PS00222; Prot_Inh_Kunz-m; 3.

RR PROSITE; PS002280; BPTI_KUNITZ_1; 3.

RR PROSITE; PS002280; BPTI_KUNITZ_2; 3.
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Q4RDL7 TETNG | Q4RDL7; | 13-SEP-2005 (; 13-SEP-2005 (; 13-SEP-2005 (; Chromosome unc
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                                                                                                                                                                                                                                                                                                                                            PS00280; BPTI_KUNITZ_1;
PS50279; BPTI_KUNITZ_2;
219 AA; 24949 MW; 81
                                                                                                                                                                                                                                 ACAKALKKKKKMPKLRFASRIRKIR
                                                                                                                                                                                                                                                                      FCSPRRDAPSFCYSPKDEGSCSASVTRYYFNIESKACEEFVYTGCGGNSNNFVKMEDCDS
                                                                                                                                                                                                                                                                                            FCAPKK-IPSFCYSFKDEGLCSANVTRYYFNPRYRTCDAPTYTGCGGNDNNFVSREDCKR
                                                                                                                                                                                                                                                                                                                                                                      RIEKVPKVCRLQVSVDDQCEGSTEKYPFNLSSMTCEKFPSGGCHRNRIENRFPDEATCMG
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                                                                                                PRELIMINARY;
                                                                                                                                                                                             -KKGSKRPRNRNRIRVPRIQ
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Pred. No. 2.5e
35; Mismatches
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5 (TrEMBLrel. 31, Created)
5 (TrEMBLrel. 31, Last sequence update)
5 (TrEMBLrel. 31, Last annotation update)
undetermined SCAF16203, whole genome shotgun

sequence.

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QSRP98
ID P98
AC QSI
AC QSI
DT 01
DT 01
DT 01
DT 01
DT HY
GN Name
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Best Local S
Matches 79
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A Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
A Micaud S., Jaffe D., Fischer S., Lutfalla G., Dossat C., Segurens B.,
A Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
A Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
A Anthouard C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
A Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
A Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
A Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
A Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
A Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
A Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
A Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
A Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
A Lindblad-Toh K., Birren B., Nusbaum C., Scarpelli C.,
A Wincker P., Lander B.S., Weissenbach J., Roest Crollius H.,
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preliminary data.

-!- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.

EMBL, CAAB01016203; CAG13515.1; -; Genomic_DNA.

InterPro; IPR002223; Prot_inh_Kunz-m.

Pfam; PP000014; Kunitz BPTI; 3.

PRINTS; PR00759; BASICPTASS.

ProDom; PD000222; Prot_Inh_Kunz-m; 3.
                                                                                                                                  OSRP98_PONPY PRELIMINARY;
OSRP98_0
01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last seq
01-FEB-2005 (TrEMBLrel. 29, Last ann
Hypothetical protein DKPZp469E1122.
Name=DKFZp469E1122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORFNames=GSTENG00038126001;
Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metozoa; Chordata; Craniata; Vertebrata; Euteleostei;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                       Pongo.
                                           Pongo pygmaeus (Orangutan).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Homin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
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PROSITE; PS50279; BPTI_KUNITZ_2; 3.
SEQUENCE 190 AA; 21614 MW; 8A7E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.1%; Score 458; DB 2; 47.6%; Pred. No. 1.1e-33; tive 28; Mismatches 55;
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annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Trpri HUMAN STANDARD; PRT; 304 AA.

11-0646; 095103;

01-JUL-1989 (Rel. 11, Created)

01-JUL-1989 (Rel. 11, Last sequence update)

13-SEP-2005 (Rel. 48, Last annotation update)

Tissue factor pathway inhibitor precursor (TPPI) (Lipoprotein-associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00014; Kunitz BPTI; 3.
PIRSF; PIRSF001620; TFPI; 1.
PRINTS; PR00759; BASICPTASB.
ProDom; PD000222; Prot Inh Kunz-m;
SMART; SM00131; KU; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osange Han M., Wiemann S.; Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
NUCLECTIDE SEQUENCE (ISOFORM ALPHA).

MEDLINE=88198127; PubMed=2452157;

Wun T.-C., Kretzmer K.K., Girard T.J., Miletich J.P., Broze G.J. Jr

"Cloning and characterization of a cDNA coding for the lipoprotein-
associated coagulation inhibitor shows that it consists of three
                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
Eukaryota; Metazoa;
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PROSITE; PS50279; BPTI_KUNITZ_2;
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inhibitor activity; IBA.
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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Bistopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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RA Raha S.S., Icquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Fahey J., Helton E., Kettenan M., Madan A., Rodrigues S., Sanchez A.,
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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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coagulation inhibitor from human plasma.",
J. Biol. Chem. 264:18832-18837(1989).
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MEDLINE=89388722; PubMed=2781520; DOI=10.1016/0049-3848(89)90454-4;
Girard T.J., Warren L.A., Novotny W.F., Bejcek B.E., Miletich J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        van der Logt C.P.B., Reitsma P.H., Bertina R.M.; "Intron-exon organization of the human gene coding for lipoprotein-associated coagulation inhibitor: the faunhibitor of the extrinsic pathway of coagulation.", Biochemistry 30:1571-1577(1991).
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J. Biol.
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FHCRC, Seattle, WA (URL: http://pga.gs.washing
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ
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SEQUENCE [GENOMIC DNA].
Saikumar N.,
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D.M., Roberts H.R.;
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Shaw N., La
                  Friedland L., Rolfe
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                                                                                                     "Characterization of human genes.";
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MEDLINE-89181950; PubMed-2927510;
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Miletich J.P., Broze G.J. Jr.;
                                                                                                                                ander B.S
                                                                                                                                                                                                                                                                                                                                                                                                                        inhibitor in complex with trypsin. Implications human mast cell tryptase and its inhibition.";
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Nakahara Y., Miyata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional significance of the Kunitz-type inhibitory lipoprotein-associated coagulation inhibitor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=15340161; DOI=10.1110/ps.(Zhang Z., Henzel W.U.; Signal peptide prediction based verified cleavage sites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Amino
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            B.S.;
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echottka G.P., Matschiner G., S
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; PubMed=8639592; DC
Hamuro T.,
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W.J.;
                                                                                                                of single-nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=2271516;
                                    er D.
Lim
                    E.P., Kalyanaraman N., I Warrington J., Lipshutz
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, Funatsu A., Miyagi M.,
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W.F., Likert K.M., Br
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RESULT 13
Q53T94 HUMAN PRELIMINARY;
ID Q53T94,
AC Q53T94,
DT 13-8EP-2005 (TrEMBLrel. 31, L.
DE Hypothetical protein TPPI.
GN Name=TPPI;
GN Name=TPPI,
OS Homo Bapiens (Human).
OC Eukaryota; Metazoa; Chordata;
OC Mammalia; Eutheria; Euarchont.
OC Homo.
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SUBCELLULAR LOCATION: Secreted.
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=Alpha; Synonyms=TFPIalpha;
IsoId=10646-1; Sequence=Displayed;
Name=Beta; Synonyms=TFPIbeta;
Name=Beta; Synonyms=TFPIbeta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P10646-2; Sequence=VSP_003030, VSP_003031; TISSUE SPECIFICITY: Mostly in endothelial cells. DOMAIN: This inhibitor contains three inhibitory domains. first domain interacts with VIIa and TP, the second one with the contains of the second one with the contains of the second one with the second one with the contains of the second one with t
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SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
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0; AAA59480.1; -; Genomic_DNA.
4; AAA59480.1; JOINED; Genomic_DNA.
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8; AAA59480.1; JOINED; Genomic_DNA.
9; AAA59480.1; JOINED; Genomic_DNA.
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9; AAA59586.1; -; Genomic_DNA.
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Pred. No. 4.3e-27;
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Best Local :
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                                                                                                                            Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
-I- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
EMBL, AC007319; AAY14807.1; -; Genomic DNA.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0030414; F:protease inhibitor activity; IEA.
GO; GO:0004867; F:serine-type endopeptidase inhibitor activity;
GO; GO:0007596; P:blood coagulation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bourne S., Stoneking T., Phillips A.; "The sequence of Homo sapiens BAC clone RP11-432D12."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases [2].
                                                                          Oryctolagus cunicul
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical SEQUENCE 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waterston
Submitted
                                                   Oryctolagus.
NCBI_TaxID=9986;
                                                                                                             Name=TFPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson R.K.
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                     TISSUB=Liver;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 LILIFLTEAALGDAAQB-------PTGNNABICLLPLDYGPCRALLLRYYYDRYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 29.7%; Score 388; DE Similarity 30.3%; Pred. No. 4.3e 86; Conservative 37; Mismatches
                                                                                                                                                                                                                                                             GNENNFTSKQECLRACKKGFIQRISKGGLIKTKRKKKQRVKIA 295
                                                                                                                                                                                                                                                                                                                                                                                                   ROCEEFIYGGCEGNONRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLE---
                                                                                                                                                                                                                                                                                                                                                                                                                QSCRQFLYGGCEGNANNFYTWEACDDACWR------IEKVPKVCRLQVSVDDQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                              GNDNNFVSREDCKRACAKAL-----
                                                                                                                                                                                                                                                                                                          NAVNNSLTPOSTKVPSLFEFHGPSWCLTPADRGLCRANENRFYYNSVIGKCRPFKYSGCG
                                                                                                                                                                                                                                                                                                                                                      CRGYITRYFYNNQTKQCERFKYGGCLGNM--NNFETLBECKNICEDGPNGFQVDNYGTQL
                                                                                                                                                                                                                                                                                                                                                                             CEGSTEKYFFNLSSMTCEKFFSGGCHRNRIENRFPDEATCMGFC------
                                                                                                                                                                                                                                                                                                                                -----APKKI------PSFCYSPKDEGLCSANVTRYYFNPRYRTCDAFTYTGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SEP-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304 AA; 35015 MW;
                                                                         cuniculus (Rabbit).
Metazoa; Chordata; Craniata;
utheria; Euarchontoglires; Gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.3e-27
                                                                          Vertebrata; Buteleostomi;
lires; Lagomorpha; Leporid
                                                                                                                                                                                                                                                                                     -KKKKKKMPKLRFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
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                                                                                                                                                                                                                                                                                     224
                                                                             Leporidae;
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MEDLINE=91057146; PubMed=2136251; Wesselschmidt R.L., Girard T.J.,

Broze

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HSSP; p10646; ITFX.

SNR; P19761; 117-173, 207-266.

SNR; P19761; 117-173; 207-266.

InterPro; IPR008296; Prot_inh_Kunz-m.

InterPro; IPR008296; Prot_inh_TPPI.

Pfam; P900014; Kunitz_BPTI; 3.

PIRSP; EIRSP001620; TFPI; 1.

PRINTS; PR00759; BASICPTASE.

PRODOM; PD000222; Prot_Inh_Kunz-m; 3.

PROSITE; PS00230; BPTI_KUNITZ_1; 3.

PROSITE; PS00279; BPTI_KUNITZ_2; 3.

Blood coagulation; Glycoprotein; Protease inlegating apprendix in the company content of the content of
 EMBL; X54708; CAA38515.1;
EMBL; 861902; AAB26836.1;
PIR; 146937; 146937.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=3377427; PubMed=8503123; DOI=10.1016/0049-3848(93)90059-W; Belaaouaj A., Kuppuswamy M.N., Birktoft J.J., Bajaj S.P.; "Revised cDNA sequence of rabbit tissue factor pathway inhibitor."; Thromb. Res. 69:547-553(1993).
-I- FUNCTION: Inhibits factor X (X(a)) directly and, in a Xa-depende way, inhibits VIIa/Tissue factor activity, presumably by forming quaternary Xa/LACI/VIIA/Tp complex. It possesses an antithrombol action and also the ability to associate with lipoproteins in plasma.
-I- SUBCELLULAR LOCATION: Secreted.
-I- DOMAIN: This inhibitor contains three inhibitory domains. The first domain interacts with VIIa and TF, the second one with Xa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WADLINE=92335027; PubMed=1630940; Warn-Cramer B.J., Broze G.J. Jr., Komiv Marn-Cramer B.J. tribett tissue factor "cDNA sequence of rabbit tissue factor Nucleic Acids Res. 20:3548-3548(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE REVISION TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids [2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (By similarity).
SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Swiss-Prot entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                long as its
                                        Reg.
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                                                                                                                                                                                                                                                                                                                                                                                                                                bitor;
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By similarity.
                                                                                                                                                                                                                       Tissue factor pathway i
BPTI/Kunitz inhibitor 1
BPTI/Kunitz inhibitor 3
BPTI/Kunitz inhibitor 3
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Reactive bond (By simil
Reactive bond (By simil
N-linked (GlcNAc. . .)
N-linked (GlcNAc. . .)
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actor pathway inhibitor.";
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NAC. . .) (Potentii
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Best Local S
Matches 89
                                                                                                                                                                                                                                                                              GO; GO:00055/6; C:extracellular region; IEA.
GO; GO:000544; F:protease inhibitor activity; IE
GO; GO:0004867; F:serine-type endopeptidase inhib
GO; GO:0004867; F:slood coagulation; IEA.
InterPro; IPR002223; Prot_inh_TPPI.
InterPro; IPR002223; Prot_inh_TPPI.
InterPro; IPR002223; Prot_inh_TPPI.
IPR00014; Kunitz BPTI; 3.
PIRSF; PIRSF001620; TFPI; 1.
PRINTS; PR00759; BASICPTASE.
PRODOM; PD000222; Prot_Inh_Kunz-m; 3.
SMART; SM00131; KU; 3.
PROSITE; PS00220; BPTI_KUNITZ_1; 3.
PROSITE; PS00280; BPTI_KUNITZ_2; 3.
                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
Cyprinus carpio (Common carp).
Rukaryota; Metazoa; Chordata; Cr
Actinopterygii; Neopterygii; Tel
Cyprinidae; Cyprinus.
NCBI_TaxID=7962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains EMBL; AP008648; AAC19410.1; -; mXNA. HSSP; P31713; 1SHP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1998 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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  101
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                                                                                                                                                                                                                Similarity
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                                            VCRLQVSVDDQ---
                                                                                           CALKXDEGPCKALKDRFYFDTDTGRCESFEYGGCQGNENNFETLQECEKMCLVKEDKSP-
                                                                                                                                          CLLPLDYGPCRALLLRYYYDRYTQSCRQFLYGGCBGNANNFYTWBACDDACW-RIBKVPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILTHQCEEFIYGGCEGNENRFESLEECKEKCARDYPKMTTKLTFQKGKPDFCFLEEDPGI
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                                                                                                                                                                                          Conservative
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DDEPGPCRGLVPRYFFDFKSQECKRFFYGGCFGN-
                                                                                                                                                                                                                                                                                     33093 MW; DF69B3D76718115E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GYITRYFYNNOSKOCERFKYGGCLGNL--NNFBSLBECKNTCENPTSD
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30.7%;
                                                                                                                                                                                                             29.6%; Score 387; DB 2
35.0%; Pred. No. 5e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----APKKI----PSFCYSPKDEGLCSANVTRYYFNPRYRT
                                            -CEGSTEKYFFNLSSMTCEKFFSGGCHRNRIENRFPDEATCMGFCAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08, Last sequence up 26, Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Craniata;
Teleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 387.5;
Pred. No. 4.
                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vertebrata; Buteleostomi;
Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .7e-27
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                                                                                                                                                                                                                                      <u>ب</u>
                                                                                                                                                                                71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibitor activity; IEA
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  ANNEKTIKECHERCLE
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Search completed: M Job time : 232 secs	₽	ş	문	ঠ	DЬ	श्च
comple ne : 23;	274	220	214	160	154	152
Search completed: March 9, 2006, 19:56:47	274 KLR 276	220 KLR 222	214 SPIDRGNCEGSEGRYMINPRIKRCOMFHYSGCGGNKNNFVKRGDCIKMCMKDLRRKLIRL 273	160 SPKDEGLCSANVTRYYENPRYRTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKMP 219	154 ALMMBRNAPLKPBEBBAKPKTBPLAKHYBAPLNASHLPMQRMSKPSAKKPRLNRPKLCP 213	

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                        seq length: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein search, using sw model
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Match
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413.378 Million cell updates/sec
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1306
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| Comb.pep:*
| Cgn2_6/ptodata/1/laa/5_COMB.pep:*
| Cgn2_6/ptodata/1/laa/6_COMB.pep:*
| Cgn2_6/ptodata/1/laa/H_COMB.pep:*
| Cgn2_6/ptodata/1/laa/BTUS_COMB.pep:*
| Cgn2_6/ptodata/1/laa/BTUS_COMB.pep:*
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           SUMMARIES
Sequence 2, Appli
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Sequence 3, Appli
Sequence 2, Appli
Sequence 6, Appli
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Sequence 25, Appli
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	20	29.4	29.7	29.7	29.7	29.7	29.7	29.7	29.7	29.7	29.7	29.7	29.7	29.7	29.7	29.7	29.7	29.7
	376	213	276	276	276	276	276	276	276	276	381	304	304	304	304	304	304	304
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	TIC_08_796_850-1	5466783-25	PCT-US95-09464-9	PCT-US95-09377-3	US-09-741-106-9	US-08-943-682-9	US-08-854-764-3	US-08-436-175-9	US-08-286-521-9	US-08-437-841-9	US-09-949-016-7400	5466783-2	US-10-167-351-1	US-09-054-272-16	US-09-638-770A-1	US-09-421-097-25	US-09-240-136-1	US-09-414-878-1
	Section 1. Appli	Patent No. 5466783	Sequence 9, Appli	Sequence 3, Appli	Sequence 9, Appli	Sequence 9, Appli	Sequence 3, Appli	Sequence 9, Appli	Sequence 9, Appli	Sequence 9, Appli	Sequence 7400, Ap	Patent No. 5466783	щ	Sequence 16, Appl	Sequence 1, Appli	Sequence 25, Appl	Sequence 1, Appli	Sequence 1, Appli

ALIGNMENTS

RESULT 1 US-08-147-710-2

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LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-147-710-2
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                                                                                                                                                                                                                                        CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PARKET, GATY E
REGISTRATION NUMBER: 31-684
REFERENCE/DOCKET NUMBER: 93-14
REFERENCE/DOCKET NUMBER: 93-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEPHONE: 206-548-2329
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
                                                                              Query Match
Best Local Similarity
Matches 235; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sprecher, Cindy A.
APPLICANT: Kisiel, Walter
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS AND
TITLE OF INVENTION: METHODS RELATING THERETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 4225 ROCITY: Seattle STATE: WA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: ZymoGenetics, Inc. STREET: 4225 Roosevelt Way, N.E.
Conservative
                                                                                 100.0%; Score 1306; DB 1;
100.0%; Pred. No. 2e-123;
tive 0; Mismatches 0;
                                                                                                                         Length 235;
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US-08-458-090-2
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                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 1306; DB 1; Best Local Similarity 100.0%; Pred. No. 2e-123; Matches 235; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
ATTORIX/AGENT INFORMATION:
ANAME: PAIKEY, GAIY B
REGISTRATION NUMBER: 31-648
REFRENCE/DOCKET NUMBER: 93-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
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APPLICANT: Kisiel, Walter
APPLICANT: FOSTER, Donald C.
TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS AND NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                              61 CRQFLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSM 120

    Application US/08458090
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RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKMFKLRFASRIRKIRKKQF
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                                                                                        TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIPSFCYSPKDEGLCSANVTRYYFNPRY 180
                                                                                                                                CROFLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLOVSVDDQCEGSTEKYFFNLSSM
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                                                      TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIPSFCYSPKDEGLCSANVTRYYFNPRY
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201 Eastlake Avenue East
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US-08-457-887-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 93-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEPHONE: 206-442-6678
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Patent No.
                                                                                                                                                                                                                                                                                            Matches 235; Conservative
                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Sprecher, Cindy A.
APPLICANT: Kisiel, Walter
APPLICANT: Kisiel, Walter
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: MOVEL HUMAN KUNITZ-TYPE INHIBITORS
TITLE OF INVENTION: METHODS RELATING THERETO
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                           Match 100.0%;
Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
181
                                  181
                                                                      121
                                                                                                       121 TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIPSFCYSPKDEGLCSANVTRYYFNPRY 180
                                                                                                                                                                           61 CRQFLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSM 120
                                                                                                                                               61
                                                                                                                                                                                                                                        1 MDPARPIGISILLLFLTEAALGDAAQEPTGNNAEICLLFLDYGFCRALLLRYYYDRYTQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seattle
                                                                      TCEKFFSGGCHRNRI ENRFPDEATCMGFCAPKKI PSFCYSPKDEGLCSANVTRYY FNPRY
                    RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKMPKLRFASRIRKIRKKQF 235
RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKKMPKLRFASRIRKIRKKQF
                                                                                                                                           CROFLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSM
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Pred. No. 2e-123;
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RESULT 4 US-08-817-145-3

Sequence 3, Application US/08817145
PATENT NO. 6025329
GENERAL INFORMATION:
APPLICANT: UTSUMI, Jun
APPLICANT: SUDO, Tetsuo

TANAKA, Yasuhiko

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                                                                                                                                                                                                                                                          US-09-702-705-332
                                                                                                                                                        Sequence 332, Application US/09702705
Patent No. 6504010
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
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                                                                                                     APPLICANT:
APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: PECENTIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,145
PILING DATE: 02-JUL-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JT., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 760-230P
                                                                  APPLICANT:
                                                APPLICANT:
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INFORMATION FOR SEQ ID NO: 3:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: THERAPEUTIC AGENT FOR OPHTHALMIC
TITLE OF INVENTION: DISEASES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
Ench, Stewart, Kolasch & Birch, ILP.
STREET: P.O. Box 747
CITY: Falls Church
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LENGTH: 235 amino acide
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TOPOLOGY: lin
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                         Wang, Tongtong
Bangur, Chaitanya S
Lodes, Michael A.
Panger, Gary
Vedvick, Tom
Carrer, Darrick
Retter, Marc
Mannion, Jane
Pan, Liqun
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Liqun
N: COMPOSITIONS AND METHODS FOR THE THERAPY AND
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APPLICANT: Pan, Lique
APPLICANT: Wang, Aijun
APPLICANTON: COMPOSITIONS AND METHODS FOR
APPLICATION: COMPOSITIONS AND METHODS FOR
APPLICATION NUMBER: US/09/736,457
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILLING DATE: 2000-12-13
ANUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows
SEQ ID NO 332
LENGTH: 235
TYPE: PRT
OPPT: PRT
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FILE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 332
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-09-702-705-332
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                                                                                                                                  Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 235; Conservative 0
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.0%;
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                            CKQFLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSM 120
                                                                  MDPARPLGLS ILLLFLTEAALGDAAQEPTGNNAEICLLFLDYGPCRALLLRYYYDRYTQS
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Lodes, Michael A.
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Pred. No. 26
                                                                                                                                  Score 1306; DB 2;
Pred. No. 2e-123;
); Mismatches 0;
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                                                                                                                                                                    Length 235;
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APPLICANT: FANGER, GARY
APPLICANT: Vedvick, Tom
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
ITITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
ITITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C9
CURRENT APPLICATION NUMBER: US/09/614,124B
CURRENT FILING DATE: 2001-07-11
NUMBER OF SEQ ID NOS: 1668
SOFTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 332
LENGTH: 235
TYPOE: DOT
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APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
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Matches
                                                                                                                                                                                                                     Sequence 2, Application US/09904621 Patent No. 6656746 GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Kisiel, Walter
APPLICANT: Fister, Donald C.
TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS
TITLE OF INVENTION: MATHODS RELATING THERETO
TITLE OF INVENTION: METHODS RELATING THERETO
FILE REFERENCE: 93-1403
CURRENT APPLICATION NUMBER: US/09/904,621
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/265,627
PRIOR FILING DATE: BARLIER FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 5,455,338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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ORGANISM: Homo sapiens
-09-614-124B-332
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Patent No. 66305
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APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Garry
APPLICANT: Vedvick, Tom
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Pan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C12
CURRENT APPLICATION NUMBER: US/09/671,325
CURRENT FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 1825
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 332
LENGTH: 235
TYPE: PAT
ORGANISM: Homo sapiens
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; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; SEQ ID NO 2
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-621-2
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GENERAL INFORMAT
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Best Local Similarity
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TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIPSFCYSPKDEGLCSANVTRYYFNPRY

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APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
ITTLE OF INVENTION: COMPOSITIONS AND METHODS FOR
ITTLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C8
CURRENT APPLICATION NUMBER: US/09/589,184
CURRENT FILING DATE: 2000-06-05
NUMBER OF SEQ ID NOS: 827
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 332
LENGTH: 235
TYPE: PRT
ORGANISM: Homo Bapiens
US-09-589-184-332
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US-09-589-184-332
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Lodes, Michael A.
APPLICANT: Panger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C11
CURRENT APPLICATION NUMBER: US/09/658,824
CURRENT FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 1788
SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-658-824-332
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APPLICANT: Bangur, Chaitanya S
APPLICANT: Lodes, Michael A.
APPLICANT: Lodes, Michael A.
APPLICANT: Panger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
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GENERAL INCORMATION:
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
ITITE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND ITITE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND ITITE OF INVENTION WIMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTMARE: FASTERQ for Windows Version 4.0
SEQ ID NO 6735
LENGTH: 235
TYPE: PRT
ORGANISM: Human
US-09-949-016-6735
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-658-824-332
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LENGTH: 235
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                       RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKKMPKLRFASRIRKIRKKQF 235
                                                                                                              TCEKFFSGGCHRURIEURFPDEATCMGFCAPKKIPSFCYSPKDEGLCSAUVTRYYFUPRY 180
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RESULT 13 US-10-017-754-332

Sequence

332,

Application US/10017754

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APPLICANT: Panger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Carter, Marc
APPLICANT: Mention, Jane
APPLICANT: Mennion, Jane
APPLICANT: PILLE COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
CURRENT APPLICATION UNMBER: US/09/651,563
CURRENT FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 1679
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 332
LENGTH: 235
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; ORGANISM: Homo sapiens
US-10-017-754-332
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CURRENT APPLICATION NUMBER: US/10/017,754
CURRENT FILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 2004
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 332
LENGTH: 235
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Best Local Similarity 100.0%;
Matches 235; Conservative (
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GENERAL INFORMATION:
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APPLICANT: Bangur, Chaitar
APPLICANT: Lodes, Michael
APPLICANT: Fanger, Gary
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APPLICANT: Wang, Tongrong
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Retter, Marc W.
APPLICANT: Marnerakis, Margarit
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Panger, Gary R.
Vedvick, Thomas S.
Bangur, Chaltanya S.
McNabb, Andria
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Lodes, Michael A.
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Pred. No. 2e-123;
D; Mismatches 0;
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Search completed: March Job time : 48 secs

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C4
CURRENT APPLICATION NUMBER: US/09/519,642
CURRENT FILING DATE: 2000-03-06
NUMBER OF SEQ ID NOS: 789
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 332
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-09-519-642-332
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; Patent No. 6933363
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US-09-651-563-332
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
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  US-09-904-621-2
US-09-9736-457-332
US-09-9476-300-332
US-09-446-3300-332
US-10-060-036-167
US-10-060-036-167
US-10-013-872-332
US-10-021-660-119
US-10-131-872-332
US-10-283-017-332
US-10-283-017-332
US-10-285-027-24
US-10-285-027-24
US-10-286-084-2
US-10-800-684-2
US-10-800-684-2
US-10-991-321-24
US-10-991-321-24
US-10-991-321-24
US-10-806-684-2
US-10-991-321-24
US-10-991-321-340-48
US-09-992-0958-48
US-09-992-0958-88
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Sequence 2, Appli
Sequence 332, App
Sequence 332, App
Sequence 332, App
Sequence 332, App
Sequence 316, App
Sequence 117, App
Sequence 119, App
Sequence 312, App
Sequence 312, App
Sequence 32, App
Sequence 7, Appli
Sequence 7, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 36, Appli
Sequence 26, Appli
Sequence 48, Appl
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JEAALGDAAQEPTGNN	-621-2 1 NO. US20020098560A1 INFORMATION: NANT: Sprecher, Cindy A. ANT: Sprecher, Cindy A. ANT: FOSTER, Walter ANT: Kisiel, Walter ANT: FOSTER, WALTER ANT: POSTER, WATE HUMAN KU OF INVENTION: NOVEL HUMAN KU OF INVENTION: NAND FINVENTION: MATHODS RELAT SPERENCE: 93-14D3 TEFERENCE: 93-14D3 TEFERENCE: 93-14D3 TEFERENCE: 93-14D3 TAPPLICATION NUMBER: US/09/ T APPLICATION NUMBER: EARLIER FILING DATE: EARLIER FILING OF SEQ ID NOS: 15 FILING DATE: TARLIER FILING OF SEQ ID NOS: 15 FRIT ISM: Homo sapiens -621-2 atch 100.0%; Sc cal Similarity 100.0%; Sc cal Similarity 100.0%; Sc cal Similarity 100.0%; Sc	394.5 30.2 291 4 US-10-000 394.5 30.2 291 4 US-10-000 394.5 30.2 291 5 US-10-118 393.5 30.1 291 3 US-09-99 393.5 30.1 291 3 US-09-99 393.5 30.1 291 4 US-10-000 393.5 30.1 291 4 US-10-000 393.5 30.1 291 4 US-10-118 393.5 30.1 291 4 US-10-118 393.5 30.1 291 4 US-10-15 398. 29.7 304 4 US-10-15 388. 29.7 304 4 US-10-75 388. 29.7 304 5 US-10-93
60 60 12 18	NHIBITORS NUMBER: 09/265,627 03-09 NUMBER: 5,455,338 11-05 DB 3; Length 235; e-116; O: Gaps 0	Sequence 48, Appl Sequence 48, Appl Sequence 48, Appl Sequence 48, Appl Sequence 52, Appl Sequence 53, Appl Sequence 69, Appl Sequence 69, Appl Sequence 54, Appl Sequence 54, Appl

RESULT 2 US-09-736-457-332 ; Sequence 332, Application US/09736457

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APPLICANT: Carter, Darrick

APPLICANT: Panger, Gary R.

APPLICANT: Panger, Gary R.

APPLICANT: Bangur, Thomas S.

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Bangur, Chaitanya S.

APPLICANT: McNabb, Andria

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

FILE REFERENCE: 210121.478C17

CURRENT APPLICATION NUMBER: US/09/902,941

CURRENT APPLICATION NUMBER: US/09/902,941

CURRENT APPLICATION NUMBER: US/09/902,941

CURRENT FILING DATE: 2001-07-10

NUMBER OF SEQ ID NOS: 2002

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 332

LENGTH: 235
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; SEQ ID NO 332
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-332
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                                                                                                                                                                                                                                               APPLICANT: Henderson, Robert A.
APPLICANT: Wang, Tongtong
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Retter, Marc W.
APPLICANT: Marnerakis, Margarita
APPLICANT: Carter, Darrick
APPLICANT: Panger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: McNabb, Andria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 332, Application US/09902941
Patent No. US20020172952A1
GENERAL INFORMATION:
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
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TYPE: PRT
ORGANISM: Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKKMPKLRFASRIRKIRKKQF 235
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Lodes, Michael A
Fanger, Gary
Vedvick, Tom
Carter, Darrick
Retter, Marc
Mannion, Jane
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APPLICANT: Wang, Aljun
APPLICANT: Wang, Tongtong
APPLICANT: Switzer, Anne
APPLICANT: Switzer, Anne
APPLICANT: Glapper, Jonathan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION NUMBER: US/09/849,626
CURRENT APPLICATION NUMBER: US/09/849,626
CURRENT APPLICATION NUMBER: US/09/849,626
CURRENT FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 1926
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 332
LENGTH: 235
TYPE: BRT
ORGANISM: Homo Bapiens
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Best Local Similarity 100.
Matches 235; Conservative
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APPLICANT: Fanger, Gary
APPLICANT: Wang, Aijun
APPLICANT: Wang, Tongtong
APPLICANT: Switzer, Anne
    181
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                                                                                                                                                                                       CRQFLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSM 120
                                        RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKMPKLRFASRIRKIRKKQF 235
RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKMPKLRFASRIRKIRKKQF
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                                                                                 TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIPSFCYSPKDEGLCSANVTRYYFNPRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKMPKLRFASRIRKIRKKQF
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RESULT 5 US-09-476-300-332 ; Sequence 332, Application US/09476300 ; Publication No. US20030125245A1

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APPLICANT: Wang, Tongtong
APPLICANT: Watenabe, Yoshihiro
APPLICANT: Watenabe, Yoshihiro
APPLICANT: Retter, Jeffrey C.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Marnerakis, Margarita
APPLICANT: Panger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Wedvick, Thomas S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: MCNAbb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C18
CURRENT APPLICATION NUMBER: US/10/017,754
CURRENT APPLICATION NUMBER: US/10/017,754
CURRENT FILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 2004
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 332
LENGTH: 235
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                                                                                    Query Match
Best Local S
Matches 235
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APPLICANT: Wangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210111.478C3
CURRENT APPLICATION UNMBER: US/09/476,300
CURRENT FILING DATE: 1999-12-30
RUMBER OF SEQ ID NOS: 785
SOFTWARE: PASESEQ for Windows Version 3.0
SEQ ID NO 332
LENGTH: 235
TYPE: DET
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Matches
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APPLICANT: Henderson, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 332, Appublication No.
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                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                             Local Similarity
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RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKMPKLRFASRIRKIRKKQF 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CROPLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYPFNLSSM
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o. US20030054363A1
                                                                                    100.0%; Score 1306; DB 4; ilarity 100.0%; Pred. No. 2.6e-116; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1306; DB 3; ilarity 100.0%; Pred. No. 2.6e-116; Conservative 0; Mismatches 0;
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Sequence 316, Application US/10097340
Publication No. US20030087250A1
GENERAL INFORMATION:
APPLICANT: John MONAHAN
APPLICANT: Wanjula GANNAVARAPU
APPLICANT: Sebastian HOERSCH
APPLICANT: Shubhangi KAMATKAR
APPLICANT: Steve G. KOVATS
APPLICANT: Rachel E. MEYERS
APPLICANT: Rachel MCRRISEY
APPLICANT: Peter CLANDT

SEN

US-10-097-340-316

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APPLICANT: Benson, Darin R.

APPLICANT: Kalos, Michael D.

APPLICANT: Lodes, Michael J.

APPLICANT: Lodes, Michael J.

APPLICANT: Persing, David H.

APPLICANT: Persing, David H.

APPLICANT: Jiang, Yuqiu

TITLS OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAE

TITLS OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER

FILE REFERENCE: 210121.566

CURRENT APPLICATION NUMBER: US/10/060,036

CURRENT APPLICATION NUMBER: US/10/060,036

CURRENT FILING DATE: 2002-01-30

NUMBER OF SEQ ID NOS: 4560

SOFTMARE: PastSEQ for Windows Version 4.0

SEQ ID NO 167

LENGTH: 235

TYDE: DET
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; ORGANISM: Homo sapiens
US-10-060-036-167
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Best Local Similarity
Matches 235; Conserv
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  RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKMPKLRFASRIRKIRKKQF 235
                        RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKKMPKLRFASRIRKIRKKQF 235
                                                                                                    TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIPSFCYSPKDEGLCSANVTRYYFNPRY 180
                                                                                                                                                            CROFLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSM
                                                                                                                                                                               CRQFLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSM 120
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                                                                              TCEKFFSGGCHRNRIENRFDDEATCMGFCAPKKIPSFCYSPKDEGLCSANVTRYYFNPRY
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100.0%; Pred. No. 2.6e-116;
ative 0; Mismatches 0;
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APPLICANT: Rosemarie SCHMANDT
APPLICANT: Xumei ZHAO
APPLICANT: Xumei ZHAO
APPLICANT: Xumei ZHAO
APPLICANT: Karen GLATT
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
TURE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR PILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR APPLICATION NUMBER: 60/323,580
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PRIOR APPLICATION NUMBER: 60/323,
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US-10-021-660-119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
APPLICANT: Mirray, Richard
APPLICANT: Mirray, Richard
APPLICANT: Matson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: EQS Biotechnology, Inc.
TITLE OF INVENTION: No. US20030152926Alel Methods of Diagnosis of Angiogenesis,
TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
TITLE OF INVENTION: Modulators
FILE REFERENCE: 018501-000710US
CURRENT APPLICATION NUMBER: US/10/021,660
CURRENT APPLICATION NUMBER: US/09/784,356
PRIOR APPLICATION NUMBER: US/09/784,356
PRIOR APPLICATION NUMBER: US 09/637,977
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ORGANISM: Homo sapiens
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Robert C. BAST, Jr.
Karen LU
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APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
FILE REFERENCE: 210121.478C19
CURRENT APPLICATION NUMBER: US/10/113,872
CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 2011
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 332
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-10-113-872-332
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US-10-021-660-119
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Best Local
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                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                             121 TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIPSFCYSPKDEGLCSANVTRYYFNPRY 180
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                                                                                                                                                 CRQPLYGGCEGNANNPYTWEACDDACWRIBKVPKVCRLQVSVDDQCEGSTEKYFFNLSSM 120
RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKKMPKLRFASRIRKIRKKQF
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Kalos, Michael D.
Sleath, Paul R.
Vedvick, Thomas S.
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181 RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKMPKLRFASRIRKIRKKQF 235

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GENERAL INFORMATION:

APPLICANT: Afar, Daniel
APPLICANT: Afaz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Glynne, Richard
APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology,
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US-10-283-017-332
; Sequence 332, App
; Publication No. 1
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SOPTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 332
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo Bapiens
US-10-283-017-332
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APPLICANT: Carter, Darrick
APPLICANT: Panger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: WCNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPERENCE: 210121.478C20
CURRENT APPLICATION NUMBER: US/10/283,017
CURRENT FILING DATE: 2002-10-28
NUMBER OF GEO TO TOWNO 1075-10-28
NUMBER OF GEO TO TOWNO 1075-10-28
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APPLICANT: Wang, Tongtong
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Kalos, Michael D.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-012500US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CRQFLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSM 120
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Retter, Marc W.
Durham, Margarit
Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKMPKLRFASRIRKIRKKQF 235
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Watanabe, Yoshihiro
Kalos, Michael D.
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o. US20030211510A1
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APPLICANT: GERBER, HANS-PETER

APPLICANT: GERBER, HANS-PETER

ITITLE OF INVENTION: VEGF-MODULATED GENES AND METHODS EMPLOYING THEM

FILE REFERENCE: 09800080-0103

CURRENT APPLICATION NUMBER: US/10/428,487

CURRENT FILING DATE: 2003-05-02

PRIOR APPLICATION NUMBER: 09/815,153

PRIOR PILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,201

PRIOR APPLICATION NUMBER: 60/191,201

PRIOR PILING DATE: 2000-03-22

NUMBER OF SEQ ID NOS: 84

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 7
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PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR PILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR PILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/34,393
PRIOR PILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR PILING DATE: 2001-11-21
PRIOR PILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR PILING DATE: 2002-01-10
PRIOR PILING DATE: 2002-01-10
PRIOR PILING DATE: 2002-01-10
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Best Local Similarity
Matches 235; Conserv
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CURRENT FILING DATE: 2002-11-13
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TYPE: PRT
ORGANISM: Homo sapiens
LENGTH: 235
TYPE: PRT
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100.0%; Pred. No. 2.6e-116;
1tive 0; Mismatches 0;
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ORGANISM: Homo sapiens

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APPLICANT: AZIZ, Natasha
APPLICANT: Bos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators
FILE REFERENCE: 018501-006200US
CURRENT APPLICATION NUMBER: US/10/211,462
CURRENT FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: US 09/784,356
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/791,390
PRIOR APPLICATION NUMBER: US 60/310,025
PRIOR APPLICATION NUMBER: US 60/334,244
PRIOR APPLICATION NUMBER: US 60/334,244
PRIOR FILING DATE: 2001-02-22
SPIOR FILING DATE: 2001-03
PRIOR FILING DATE: 2001-03
SPIOR FILING DATE: 2001-05: 230
SOFTWARE: Patentin Ver. 2.1
SEQ ID NOS: 230
SOFTWARE: Patentin Ver. 2.1
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US-10-211-462-52
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Best Local S
Matches 235
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APPLICANT: Glynne, Richard
APPLICANT: Watson, Susan F
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                       h 100.0%; Score 1306; DB 4; Length 235; Similarity 100.0%; Pred. No. 2.6e-116; 35; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                               CRQFLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSM 120
                                                                                                                                                                  CRQFLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSM 120
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                          RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKMPKLRFASRIRKIRKKOF 235
                                                                             TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIPSFCYSPKDEGLCSANVTRYYFNPRY
                                                                                                             TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIPSFCYSPKDEGLCSANVTRYYFNPRY 180
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Watson, Susan R.
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APPLICANT: KISICH, WAITER
APPLICANT: KISICH, WAITER
APPLICANT: KISICH, WAITER
APPLICANT: KISICH, WAITER
APPLICANT: FOSTER, CONALD C.
APPLICANT: FOSTER, DONALD C.
TITLE OF INVENTION: MOVEL HUMAN KUNITZ-TYPE INHIBITORS
TITLE OF INVENTION: METHODS RELATING THERETO
FILE REFERENCE: 93-14D3
CURRENT APPLICATION HUMBER: US/10/680,684
CURRENT FILING DATE: 2003-10-07
FRIOR APPLICATION NUMBER: US/99/904,621
PRIOR APPLICATION NUMBER: US/99/904,621
PRIOR FILING DATE: POIDE APPLICATION NUMBER: 09/265,627
PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: 99/265,627
PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: 5,455,338
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-680-684-2
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Publication No. US20040253686A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 1306; DB 5; Best Local Similarity 100.0%; Pred. No. 2.6e-116;
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181
                                                                                                                                                            121
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                                                                                                                                                   TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIPSFCYSPKDEGLCSANVTRYYFNPRY 180
TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIPSFCYSPKDEGLCSANVTRYYFNPRY 180
                                               RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKMPKLRFASRIRKIRKKQF 235
                                                                                                                                                                                                                                                                                                                            CROPLYGGCEGNANNPYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYPPNLSSM
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RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKMPKLRFASRIRKIRKKQF
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Search completed: March 9, 2006, 20:11:33 Job time : 167 secs

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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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Published Applications AA New:*

1: /cgm2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

2: /cgm2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

3: /cgm2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

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6: /cgm2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

7: /cgm2_6/ptodata/1/pubpaa/USO1_NEW_PUB.pep:*

8: /cgm2_6/ptodata/1/pubpaa/USO1_NEW_PUB.pep:*
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Gapop 10.0 , Gapext 0.5
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1306
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIBS

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	Sequence 16, Appl Sequence 21, Appl	` >	,,	Sequence 618, App	Sequence 45, Appl	44,	1619	38,		54,	1123	47,		922	450	Sequence 5, Appli	15,	Sequence 6, Appli	Sequence 1398, Ap	Description

RESULT 2
US-11-183-555-6
; Sequence 6, Application US/11183555
; Publication No. US20060025329A1

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181 R	121 T 121 T	5 T9	x-x 	1tch	NUMBER OF SE SOFTWARE: pt SEQ ID NO 139 LENGTH: 235 TYPE: PRT ORGANISM: H S-10-821-234-1	NT APPLING APPLICATIONS	APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: TITLE OF INV	1-234-1 ce 1398 ation M		78 77.5	79 78	80.5 79	82 81	83.5 82	83.5	86	•	86.5	888	2
TCDAFTYI TCDAFTYI	CEKFFSGG CEKFFSGG	ROFLYGGO ROFLYGGO	MDPARPLGLS MDPARPLGLS	Similarity S; Conservat	NUMBER OF SEQ ID NOS: 1704 SOFTWARE: pt SEQ_genes Versio EQ ID NO 1398 LENGTH: 235 TYPE: PRT ORGANISM: Homo sapiens 10-821-234-1398	CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 2004-0 PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2003-04-0	CANT: Meache-Crain, B: CANT: Stache-Crain, B: CANT: Andarmani, Susan CANT: Tang, Y. Tom CANT: Tang, Y. Tom BRFERRYCE: 821A	SULT 1 -10-221-234-1398 Sequence 1398, Application US/10821234 Publication No. US20050255114A1 GENERAL INFORMATION:											n 6 9	
recegnant	CHRNRII	CEGNANNI CEGNANNI	SILLLFI	100 100 vative	3: 1704 nes Version lens	NUMBER: US/ : 2004-04-0 : 2004-04-0 JMBER: US 60 2003-04-07	-Crain, Bi -Crain, Bi nani, Susan Y. Tom Y. Methods	pation ()5025511		1664 365	721 1620	2923 243	4544 340	3717 4544	3714	1013	1001	3597	1012	2
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RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKXMPKLRFASRIRKIRKKQF 	TCEKFFSGGCHRNRIENRFPDBATCMGFCAPKKIPSFCYSPKDBGLCSANVTRYYFNPRY 	CROFLYGGCEGNANNFYTWEACDDACWRIEKVDKVCRLQVSVDDQCEGSTEKYFFNLSSM 	MDPARPLGLSILLLFLTEAALGDAAQEPTGNNAEICLLFLDYGPCRALLLRYYYDRYTQS 	Score 1306; Pred. No. 3.7 ; Mismatches		., 234)47	osis and		ALIGNMENTS	055-877-21 108-528-56	22-478-1 55-877-2	12-109-2	76-427A- 26-657-1	01-035-2	95-561-1	US-10-131-826A-38 US-10-973-115B-38	US-11-019-711-2 US-11-132-285-40	19-711-6	53-372-6	3-393-6
KTX4WDXTX	PSFCYSPR	WCRLQVSV	CTT PTDA	DB 6; I .7e-122; B 0; I			Treatment			6	13	ω ·	74	14	015	388	0		0.0	•
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TITLE OF INVENTION: Compositions and Methods for Inhibiting Cellular Proliferation
TITLE OF INVENTION: Composition TrPI Pragments
FILE REFERENCE: 05213-0297 (43)70-300210)
CURRENT APPLICATION NUMBER: US/170-300210
CURRENT FILING DATE: 2005-07-18
PRIOR APPLICATION NUMBER: US 09/766,778
PRIOR PILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: US 09/227,955
PRIOR APPLICATION NUMBER: US 09/36,850
PRIOR APPLICATION NUMBER: US 09/36,850
PRIOR APPLICATION NUMBER: US 09/30,273
PRIOR APPLICATION NUMBER: US 09/130,273
PRIOR PILING DATE: 1998-08-06
SOFTMARE: Patentin version 3.3
SEQ ID NO6: 6
SOFTMARE: Patentin version 3.3
TYPE: PRT
                                                                      ; ORGANISM: Homo sapiens US-10-821-234-1540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1540, Application US/10821234 Publication No. US20050255114A1 GENERAL INFORMATION:
                                                                                                                                     SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 1540
LENGTH: 304
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Best Local Similarity
Matches 213; Conserv
Query Match
Best Local Similarity
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APPLICANT: Hembrough, Todd
APPLICANT: Papathanassiu,
                                                                                                                                                                                                                                                                                FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and
                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 1704
                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/462,047 PRIOR FILING DATE: 2003-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Stache-Crain, Birgit
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Labat, Ivan
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APPLICANT: Green, Shawn J.
                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 ATCMGFCAPKKIPSFCYSPKDEGLCSANVTRYYFNPRYRTCDAFTYTGCGGNDNNFVSRE 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDACWRIEKVEKVCRLQVSVDDQCEGSTEKY FENLSSMTCEKFFSGGCHRNRIENRFEDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DCKRACAKALKKKKMPKLRPASRIRKIRKKQP 213
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29.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91.9%; Score 1200; DB 7; Length 213; 100.0%; Pred. No. 1.1e-111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adonia B.
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Score
Pred.
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388; DB 6;
No. 4.3e-31;
                                                                                                                                                                                                                                                                                                                                                       Treatment of Preeclampsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                     Length 304;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: US-11-183-555-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
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                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Papathanassiu, Adonia E.
APPLICANT: Green, Shawn J.
TITLE OR INVENTION: Compositions and Methods for Inhibiting Cellular Proliferation
TITLE OF INVENTION: Comprising TFPI Fragments
FILE REFERENCE: 05213-0297 (43170-300210)
CURRENT APPLICATION NUMBER: US/11/183,555
CURRENT FILING DATE: 2005-07-18
PRIOR APPLICATION NUMBER: US 09/766,778
PRIOR PRIOR APPLICATION NUMBER: US 09/766,778
PRIOR PRIOR APPLICATION NUMBER: US 09/227,955
PRIOR FILING DATE: 2001-01-22
PRIOR FILING DATE: 1999-01-11
PRIOR FILING DATE: 1999-01-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 08/796,850
PRIOR FILING DATE: 1997-02-06
PRIOR APPLICATION NUMBER: US 09/130,273
PRIOR FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hembrough, Todd
APPLICANT: Papathanassiu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 276
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                           170
                                                                                    141 BECKNICEDGPNGFQVDNYGTQLNAVNNSLTPQSTKVPSLFBFHGPSWCLTPADRGLCRA 200
                                                                                                                                 143 ATCMGFC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193
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                                                                                                                                                                          86 KTTLQQEKPDFCFLE---EDPGICRGYITRYFYNNQTKQCERFKYGGCLGNM--NNFETL 140
                                                                                                                                                                                                               89 ----IEKVPKVCRLQVSVDDQ--CEGSTEKYFFNLSSMTCEKFFSGGCHRNRIENRFPDE 142
                                                                                                                                                                                                                                                               26 CAFKADDGPCKAIMKRFFFNIFTRQCESFIYGGCEGNQNRFESLEECKKMCTRDNANRII 85
                                                                                                                                                                                                                                                                                     36 CLLPLDYGPCRALLLRYYYDRYTQSCRQPLYGGCEGNANNFYTWEACDDACWR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 LLLNLAPAPLNADSBEDBEHTIITDTELPPLKLMHSFCAFKADDGPCKAIMKRFFFNIFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 LILFLTEAALGDAAQE------PTGNNAEICLLFLDYGFCRALLLRYYYDRYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66;
                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                  NVTRYYFNPRYRTCDAFTYTGCGGNDNNFVSREDCKRACAKAL-------KKKKK 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNENNFTSKQECLRACKKGFIQRISKGGLIKTKRKKKQRVKIA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNDNNFVSRBDCKRACAKAL------KKKKKMPKLRFA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAVNNSLTPOSTKVPSLFEFHGPSWCLTPADRGLCRANENRFYYNSVIGKCRPFKYSGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----APKKI-----PSFCYSPKDEGLCSANVTRYYFNPRYRTCDAFTYTGCG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CEGSTEKY FFNLSSMTCEKFFSGGCHRNRIENR FPDEATCMGFC--------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRGYITRYFYNNQTKQCERFKYGGCLGNM--NNFETLEBCKNICEDGPNGFQVDNYGTQL
NENR FYYNSVIGKCR PFKYSGCGGNENN FTSKQECLRACKKG FIQRISKGGLIKTKRKRK
                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic peptide
                                                                                                                                                                                                                                                                                                                                                 29.4%; Score 384.5; DB 7 31.6%; Pred. No. 8.6e-31; tive 35; Mismatches 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37;
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                                                                                                                               ---APKKI------PSFCYSPKDEGLCSA 169
                                                                                                                                                                                                                                                                                                                                                                                            DB 7;
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                                                                                                                                                                                                                                                                                                                                                   Indels 63;
                                                                                                                                                                                                                                                                                                                                                                                            Length 276;
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260
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218 MPKLRFA 224 ::: | 261 KQRVKIA 267

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ASULT 6

JS-11-000-463

Sequence 922, Ay-
Publication No. US20.

GENERAL INFORMATION:
APPLICANT: Tang, Y Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Chen, Rui-hong
PLICANT: Qian, Xiaohong B.

"CANT: Wang, Zhiwei
Wehrman, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Webtran, Tom
APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Zhou, Ping
APPLICANT: Cao, Yi-Cheng
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: NOVEL Nucleic Acids and Polypeptides
FILE REFERENCE: 785CIP4CN
FILE APPLICATION NUMBER: US/11/000,463
CURRENT APPLICATION NUMBER: US/21,265
PRIOR APPLICATION NUMBER: 10/291,265
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 09/922,279
PRIOR APPLICATION NUMBER: 09/922,279
PRIOR APPLICATION NUMBER: 09/922,279
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-09-15
PRIOR PILING DATE: 2000-09-15
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US-11-000-463-450
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US-11-000-463-450
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SEQ ID NO 450
LENCTH: 352
TYPE: PRT
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APPLICANT: Liu, Chenghua
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 13.8%; Score 180; DB 7
Local Similarity 35.0%; Pred. No. 2e-10;
Les 42; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                224 VTKKEDSCQLGYSA-GPCMGMTSRYFYNGTSMACETFQYGGCMGN--GNNFVTEKECLQT 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 CAPKKIPSFCYSPKDEGLCSANVTRYYFNPRYRTCDAFTYTGCGGNDNNFVSREDCKRAC 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 IEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSMTCEKFFSGGCHRNRIENRFPDEATCMGF 148
                                                                                                                                                                                                                                                                                                                                                                                                                               C---RTVAACNLPIVRGPCRAFIQLWAFDAVKGKCVLFPYGGCQGNGNKFYSEKECREYC 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen, Rui-hong
Qian, Xiaohong B.
Wang, Zhiwei
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o. US20050266423A1
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PRIOR APPLICATION NUMBER: 60/586,856
PRIOR PILING DATE: 2004-07-09
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
EEQ ID NO 28
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-11-177,506-28
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TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 785CIP4CN
CURRENT APPLICATION NUMBER: US/11/000,463
CURRENT FILING DATE: 2004-11-29
PRIOR APPLICATION NUMBER: 10/291,265
PRIOR FILLING DATE: 2002-11-08
PRIOR FILLING DATE: 2001-01-25
PRIOR PILLING DATE: 2001-01-25
PRIOR FILLING DATE: 2001-08-03
PRIOR FILLING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR APPLICATION NUMBER: 09/613,451
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR APPLICATION NUMBER: 09/631,451
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; ORGANISM: Homo sapiens
US-11-000-463-922
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NUMBER OF SEQ ID NOS: 944
SOFTWARE: PastSEQ for Windows Version
SEQ ID NO 922
LENGTH: 352
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                                                                           Matches
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Best Local Similarity
Matches 42; Conserv
                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Beyer, Wayne F.
APPLICANT: Venetta, Thomas M.
APPLICANT: Groelke, John W.
APPLICANT: Blaesius, Rainer H.
APPLICANT: Blaesius, Rainer H.
APPLICANT: Blaesius AND COMPOSITIONS FOR THE
TITLE OF INVENTION: DETECTION OF OVARIAN DISEASE
FILE REFERENCE: 46.143/294851
CURRENT APPLICATION NUMBER: US/11/177,506
CURRENT FILING DATE: 2005-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 09/633,870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      281 C---RTVAACNLPIVRGPCRAFIQLWAFDAVKGKCVLFPYGGCQGNGNKFYSEKECREYC 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 CAPKKIPSFCYSPKDEGLCSANVTRYYFNPRYRTCDAFTYTGCGGNDNNFVSREDCKRAC 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 VIKKEDSCQLGYSA-GPCMGMTSRYFYNGTSMACETFQYGGCMGN--GNNFVTEKECLQT 280
89 IEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSMTCEKKFFSGGCHRNRIENRFPDEATCMGF 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 IEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSMTCEKFFSGGCHRNRIENRFPDEATCMGF 148
                                                                           42;
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Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/11177506
No. US20060029956A1
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Cao, Yi-Cheng
                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.8%; Score 180; DB 7
35.0%; Pred. No. 2e-10;
ative 14; Mismatches
                                                                      13.8%; Score 180; DB 7; Length 352; 35.0%; Pred. No. 2e-10; tive 14; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 7; Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58;
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                                                                         Gaps
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US-11-137-465-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US/10/239,663
PRIOR PLING DATE: 2002-09-24
PRIOR PLING DATE: 2002-09-25
PRIOR PPLICATION NUMBER: PCT/US01/09226
PRIOR PPLICATION NUMBER: 60/192,158
PRIOR PPLICATION NUMBER: 60/192,668
PRIOR PILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 60/192,668
PRIOR APPLICATION NUMBER: 60/200,166
                                                                                                                                                                                                                                                          Sequence 1123, Application US/10821234 Publication No. US20050255114A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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Publication No. US20050255558A1
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
                                                                                                                                  APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
                                                                                                                                                                                                            APPLICANT: Labat, APPLICANT: Stach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: GP50018
CURRENT APPLICATION NUMBER: US/11/137,465
CURRENT FILING DATE: 2005-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kabnick, Karen
TITLE OF INVENTION: NOVEL COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Agarwal, Pankaj
APPLICANT: Murdoch, Paul
                                                                                                                      FILE REFERENCE: 821A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                         460 EDVLKDDKMGLKFLGTK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  401 SRESCEDAC-PVPRTPPCRACRIRSKLALSICRSDFAIVGRITEVLEEPEAAGGIARVAL 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              345 EACQQACARGP----GDACVLPAVQGPCRGWEPRWAYSPLLQQCHPFVYGGCEGNGNNFH 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281 C---RTVAACNLPIVRGPCRAFIQLWAFDAVKGKĆVLFPYGGCQGNGNKFYSEKECREYC 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 TWEACDDACWRIEKVP--KVCRLQVSVDDQCEGSTEKYFFNLSSMTCEKFFSGGCHRNRI 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 EAALGDAAQEPTGNNAEICLLPLDYGPCRALLLRYYYDRYTQSCRQFLYGGCEGNANNFY 77
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Rizvi, Safia, K.
Smith, Randall, F.
Xiang, Zhaoying
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                                                                                                                                                                                                               Stache-Crain, Birgit
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Pred. No. 3.6e-10;
1; Mismatches 64;
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; TYPE: PRT
; ORGANISM: Homo mapiens
US-10-821-234-1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-11-068-783-54
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US-11-068-783-54
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PRIOR FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 113
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 54
LENGTH: 58
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 1123
LENGTH: 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/10982545 Publication No. US20050244890A1
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Best Local :
                                                                                                                                                                                                                                           APPLICANT: Simonsen, Anja Hviid
APPLICANT: Blennow, Kaj
APPLICANT: Blennow, Kaj
APPLICANT: Podust, Vladdmir
APPLICANT: Ciphergen Biosystems, Inc.
TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
FILE REFERENCE: 016866-011550US
CURRENT APPLICATION NUMBER: US/10/982,545
CURRENT FILING DATE: 2004-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Burian, Jan
APPLICANT: Bartfeld, Daniel
TITLE OF INVENTION: EFFICIENT METHODS FOR PRODUCING
TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES IN HOST CELLS
FILE REFERENCE: 660081.411
                                   PRIOR APPLICATION NUMBER: US 60/526,753
PRIOR FILING DATE: 2003-12-02
PRIOR APPLICATION NUMBER: US 60/546,423
PRIOR FILING DATE: 2004-02-19
PRIOR APPLICATION NUMBER: US 60/547,250
PRIOR FILING DATE: 2004-02-23
PRIOR APPLICATION NUMBER: US 60/558,896
PRIOR APPLICATION NUMBER: US 60/558,896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/11/068,783
CURRENT FILING DATE: 2005-02-28
                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/518,360 PRIOR FILING DATE: 2003-11-07
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Davies, Huw Alun APPLICANT: McGuire, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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APPLICATION NUMBER: US 60/572,617
                     FILING DATE: 2004-04-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 PSFCYSPKDEGLCSANVTRYYFNPRYRTCDAFTYTGCGGNDNNFVSREDCKRACAKA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 CYSPKDEGLCSANVTRYYFNPRYRTCDAFTYTGCGGNDNNFVSREDCKRACAKALKK 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDFCLEPPYTGPCKARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCMRTCGGA 58
                                                                                                                                                                                                                                                                                                                                                                                                                               McGuire, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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43.9%; Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 146; DB 7;
Pred. No. 7.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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PRIOR FILING DATE: 2004-05-18
PRIOR APPLICATION NUMBER: US 60
PRIOR FILING DATE: 2004-07-08
NUMBER OF SEQ ID NOS: 16
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 770
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
PEATURE:

NAME/KEY: PEPTIDE

LOCATION: (740)..(770)

OTHER INFORMATION: C31

10-982-545-15
                                                                                                              PEATURE:
NAME/KEY: PEPTIDE
NAME/KEY: PEPTIDE
(721)..(770)
                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: PEPTIDE
LOCATION: (688)..(711)
OTHER INFORMATION: P3(40)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: PEPTIDE
LOCATION: (672)..(711)
OTHER INFORMATION: biomarker peptide 4330 Da, fragment of Amyloid
OTHER INFORMATION: beta A4 precursor, beta-amyloid protein 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: PEPTIDE
LOCATION: (672)..(713)
OTHER INFORMATION: beta-amyloid protein 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (1)..(40)
OTHER INFORMATION: biomarker peptide 4320 Da (IMAC-Ni), A-beta 1-40
OTHER INFORMATION: peptide fragment of Amyloid beta A4 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Amyloid beta A4 precursor (APP, ABPP), isoform a, protease OTHER INFORMATION: nexin II (PN-II), cerebral vascular amyloid peptide (CVAP), OTHER INFORMATION: amyloid-beta protein, beta-amyloid peptide, A4 amyloid protein, OTHER INFORMATION: Alzheimer's disease amyloid protein
                                                                                                                                                                                                    LOCATION: (714)..(770)
OTHER INFORMATION: gamma-CTF(57)
                                                                                                                                                                                                                                                                                               LOCATION: (712)..(770)
OTHER INFORMATION: gam
                                                                                                                                                                                                                                                                                                                     NAME/KEY: PEPTIDE LOCATION: (712)..
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LOCATION: (688)..(770)
OTHER INFORMATION: C83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: PEPTIDE LOCATION: (672)..(770) OTHER INFORMATION: C99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAMB/KEY: PEPTIDE
LOCATION: (18)..(687)
OTHER INFORMATION: soluble APP-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (1)..(17)
OTHER INFORMATION: signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FBATURE:
NAMB/KEY: SIGNAL
                                                                                                         OTHER INFORMATION: gamma-CTF(50)
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OTHER INFORMATION:
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LOCATION: (714)..
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N: P3(42)
                                                                                                                                                                                                                                                                                               gamma-CTF (59)
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APPLICANT: Basi, Guriq
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Yednock, Ted
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
FILE REPERENCE: ELN-002CP
CURRENT APPLICATION NUMBER: US/10/789,273
CURRENT FILING DATE: 2004-02-27
PRIOR APPLICATION NUMBER: US/10/388,389
PRIOR FILING DATE: 2003-03-12
PRIOR FILING DATE: 2003-03-12
PRIOR FILING DATE: 2003-12-06
PRIOR APPLICATION NUMBER: US 60/251,892
PRIOR PILING DATE: 2000-12-06
PRIOR FILING DATE: 2000-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPB: PRT
; ORGANISM: Homo sapiens
US-10-789-273-38
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                                                                             ; LENGTH: 763
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
US-10-821-234-1619
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Best, Local S
Matches 25
                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 1619
LENGTH: 763
                                                                                                                                                                                                                                                                                                                                                                               Sequence 1619, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
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GENERAL INFORMATION:
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 38
LENGTH: 770
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Best Local Similarity
Matches 25; Conserv
                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                     APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 821A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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10.0%; Score 130;
28.6%; Pred. No. 4
ative 17; Mismatch
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Pred. No. 3.3e-06;
6; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 141; DB 6;
Pred. No. 3.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                    4e-05;
                                       DB 6; Length 763;
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Matches

34;

Conservative

Indels

20;

Gaps

26 QEPTGNNAEICLLFLDYGFCRALLLRYYYDRYTQSCRQFLYGGCEGNANNFYTWEACDDA 85

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Sequence 45, Application US/11137465
Publication No. US2005025558A1
GENERAL INFORMATION:
APPLICANT: Agarwal, Pankaj
APPLICANT: Murdoch, Paul R.
APPLICANT: Rizvi, Safia, K.
APPLICANT: Rizvi, Safia, K.
APPLICANT: Xiang, Zhaoying
APPLICANT: Xiang, Zhaoying
APPLICANT: Kabnick, Karen
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50018
CURRENT APPLICATION NUMBER: US/11/137,465
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US/10/239,663
PRIOR FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/US01/09226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: KADNICK, KATEN
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50018
CCURRENT APPLICATION NUMBER: US/11/137,465
CCURRENT APPLICATION NUMBER: US/10/239,663
PRIOR APPLICATION NUMBER: US/10/239,663
PRIOR FILING DATE: 2001-09-24
PRIOR FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: BC/1/US01/09226
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/192,158
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: 60/192,668
PRIOR FILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: 60/200,166
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 44
LENGTH: 353
TYPE: PRT
ORGANISM: Homo sapiens
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Publication No. US2005025558A1
GENERAL INFORMATION:
APPLICANT: Agarwal, Pankaj
APPLICANT: Murdoch, Paul R.
APPLICANT: Rizvi, Safia, K.
APPLICANT: Smith, Randall, F.
APPLICANT: Smith, Randall, F.
APPLICANT: Smith, Randall, F.
APPLICANT: Smith, Randall, F.
APPLICANT: Xiang, Zhaoying
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US-11-137-465-44
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Matches 22; Conserv
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; PRIOR FILING DATE: 2001-03-22; PRIOR APPLICATION NUMBER: 60/192,158; PRIOR APPLICATION NUMBER: 60/192,668; PRIOR APPLICATION NUMBER: 60/192,668; PRIOR PILING DATE: 2000-03-27; PRIOR PILING DATE: 2000-03-27; PRIOR PILING DATE: 2000-04-27; NUMBER OF SEQ ID NO 45

; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 45
; SEQ ID NO 45
; LENGTH: 448; Pred. No. 7.3e-05; PRIOR NUMBER: 448; Pred. No. 7.3e-05; PRIOR PILING SEMILARITY SIMILARITY PRED. NO. 7.3e-05; PRIOR PILING PRIOR PRI
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Database
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Maximum DB
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq length: 0 seq length: 2000000000
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Gapop 10.0 ,
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1306
1 MDPARPLGLSILLLELTEAA......
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(without alignments)
573.780 Million cell updates/sec
        7861189 seqs, 1381955077 residues
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Listing first 45 summaries
/cgn2_6/ptodata/1/paa/US086_COMB.pep:*
/cgn2_6/ptodata/1/paa/US073_COMB.pep:*
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/cgm2_6/ptodata/1/paa/US605_COMB.pep:*
/cgm2_6/ptodata/1/paa/US607_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Score Query THE THE TENT OF T Length B PCT-US02-02781-167 PCT-US02-04915-52 PCT-US02-04915-52 PCT-US02-0782-1316 PCT-US02-0782-316 PCT-US02-34777-332 PCT-US02-34777-332 PCT-US02-34777-332 PCT-US02-3476-300-332 US-09-360-466-353-32 US-09-560-466-332 US-09-560-466-332 US-09-760-4471-41 PUS-09-760-4471-41 PUS-09-760-447-41 PUS-09-760-447-41 PUS-09-760-447-41 PUS-09-760-447-41 PUS-09-760-447-332 PUS-09-760-447-332 PUS-09-760-447-332 PUS-09-760-447-332 PUS-09-760-460-119 PUS-09-902-941-332 PUS-10-021-660-167 PUS-10-130-1388-202 PUS-10-130-1388-202 PUS-10-131-462-52 PUS-10-211-462-52 PUS-10-211-462-52 PUS-10-211-462-52 PUS-10-211-462-52 PUS-10-211-462-52 PUS-10-211-462-52 PCT-US02-680-684-2 PUS-10-211-680-684-2 PUS-10-940-774-6735 PUS-1171 ㅂ Sequence 167, App Sequence 316, App Sequence 318, App Sequence 318, App Sequence 4, App11 Sequence 4, App11 Sequence 332, App Sequence 312, App Sequence 1124, App Sequence 1119, App Sequence 96446, A Sequence 911, App Sequence 1119, App Sequence 1119, App Sequence 1119, App Sequence 1119, App Sequence 117, App Sequence 167, App Sequence 167, App Sequence 202, App Sequence 174, App Sequence 764, App Sequence 764, App Sequence 764, App Sequence 776, App Sequence 776, App Sequence 1124, App Sequence 1127, App Sequence 1128, App Sequence 1129, App Sequence 1138, App Sequence 6735, Ap Sequence 1190, App Sequence 1171, A Description

ALIGNMENTS

RESULT 1
PCT-US02-02781-167
; Sequence 167, Application PC/TUS0202781
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation

```
APPLICANT: Benson, Darin R.

APPLICANT: Kalos, Michael D.

APPLICANT: Lodes, Michael J.

APPLICANT: Lodes, Michael J.

APPLICANT: Persing, David H.

APPLICANT: Hepler, William T.

APPLICANT: Jiang, Yuqiu

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER

FILE REFERENCE: 2010121.566PC

CURRENT APPLICATION UNUMBER: PCT/US02/02781

CURRENT FILING DATE: 2002-01-30

NUMBER OF SEQ ID NOS: 4560

SOFTWARE: F86USEQ for Windows Version 4.0

SEQ ID NO 167

JENOTH: 235
                          PRIOR APPLICATION NUMBER: US 09/794,356
PRIOR FILING DATE: 2001-02-14
PRIOR PELICATION NUMBER: US 09/791,390
PRIOR FILING DATE: 2001-02-22
PRIOR PELICATION NUMBER: US 60/285,475
PRIOR APPLICATION NUMBER: US 60/285,475
PRIOR PILING DATE: 2001-04-19
PRIOR PELICATION NUMBER: US 60/310,025
PRIOR PELICATION NUMBER: US 60/350,666
PRIOR PELICATION NUMBER: US 60/350,666
PRIOR PELICATION NUMBER: US 60/350,666
PRIOR PELICATION NUMBER: US 60/334,244
PRIOR APPLICATION NUMBER: US 60/334,244
PRIOR PELICATION NUMBER: US 60/334,244
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR PELICATION NUMBER: US 60/3
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PCT-US02-04915-52
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; ORGANISM: Homo sapiens
PCT-US02-02781-167
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GENERAL INFORMATION:
APPLICANT: Murray, Richard
APPLICANT: Glynne, Richard
APPLICANT: Watson, Susan R.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Aziz, Natasha
APPLICANT: Eos Biotechnology, Inc.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators
FILE REFERENCE: 018501-006200FC
CURRENT APPLICATION NUMBER: PCT/US02/04915
CURRENT FILING DATE: 2002-02-14
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PCT-US02-07826-316
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PRIOR PILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR PILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR PILING DATE: 2001/03/26
PRIOR PILING DATE: 2001/03/26
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GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc. et al.
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
FILE REFERENCE: MRI-030PC
CURRENT APPLICATION NUMBER: PCT/US02/07826
; CURRENT FILING DATE: 2002-03-14
; CURRENT FILING DATE: 2002-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR FILING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOUTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 316
LENGTH: 235
                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 1306; DB 1; Best Local Similarity 100.0%; Pred. No. 7.7e-138; Matches 235; Conservative 0; Mismatches 0;
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Best Local Similarity
Matches 235; Conserv
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PRIOR TLING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR FILING DATE: 2001-09-26
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                                                                                                                                                                   CROFLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSM
                      RTCDAFTYTGCGGIDINIFVSREDCKRACAKALKKKKKMPKLRFASRIRKIRKKQF
                                                                                                                                                                                           CRQ#LYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKY #FNLSSM
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RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKMPKLRFASRIRKIRKKQF
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PCT-US94-12609-2
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/ ORGANISM: Homo sapiens
PCT-US02-34777-332
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CURRENT APPLICATION NUMBER: PCT/US02/34777
CURRENT FILING DATE: 2002-10-28
NUMBER OF SEQ ID NOS: 2157
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 332
LENGTH: 235
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GENERAL INFORMATION:
APPLICANT: Corixa Corporation
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GENERAL INFORMATION:
APPLICANT: ZymoGenetics, Inc.
APPLICANT: 1201 Eastlake Avenue E.
APPLICANT: Seattle
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Best Local Similarity 100.0%;
Matches 235; Conservative 0
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APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Mangur, Chaitanya S.
APPLICANT: McNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
APPLICANT: Albuquerque APPLICANT: NM
APPLICANT: US
APPLICANT: 87131
TITLE OF INVENTION: MOVE TITLE OF INVENTION: METH NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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Albuquerque
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1201 Eastlake Avenue East
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abe, Yoshihiro
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                                             NOVEL HUMAN KUNITZ-TYPE INHIBITORS AND METHODS RELATING THERETO
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pred. No. 7.7e-138;
0; Mismatches 0;
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Best Local Similarity
Matches 235; Conserv
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 93-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
                 MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                       APPLICANT: Rao, Chilukuri N.
APPLICANT: Woodley, David T.
TITLE OF INVENTION: USES OF SERINE PROTEASE INHIBITORS
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSE: Zym
STREET: 1201 E
CITY: Seattle
STATE: WA
                                                                                                                                                                                 STREET: 1700 Lincoln Street,
CITY: Denver
STATE: Colorado
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 98102
                                                                                                                                              COUNTRY: U
ZIP: 80203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                ADDRESSEE: Sheridan Ross P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
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                                                                                                                                                                                                                                                                                                                                                                                             Application US/08800483
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                                                                                                                                                                  USA
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US/08/800,483
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                                                                                                                                                                                                                               Suite 3500
                                         Version #1.30
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FILING DATE: 14 CLASSIFICATION:

14-FEB-1997

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APPLICANT: Sprecher, Cindy A.

APPLICANT: Kisiel, Walter

APPLICANT: Kisiel, Walter

APPLICANT: FOSTER, Donald C.

TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS AND TITLE OF INVENTION: METHODS RELATING THERETO FILE REFERENCE: 93-14D3

CURRENT APPLICATION NUMBER: US/09/265,627A

CURRENT FILING DATE: 1999-03-09

EARLIER APPLICATION NUMBER: 5,914,315

EARLIER APPLICATION NUMBER: 5,914,315

EARLIER APPLICATION NUMBER: 5,455,338

EARLIER FILING DATE: 1995-06-01

EARLIER FILING DATE: 1993-11-05

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 2

LENGTH: 235

TYPE: PAT

ORGANISM: Homo sapiens
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US-09-265-627-2
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US-08-800-483-4
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Best Local S
Matches 235
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NAME: Crook, Wainell M.
REGISTRATION NUMBER: 31,071
REFERENCE/DOCKET NUMBER: 3501-17
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEPAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Applicat GENERAL INFORMATION:
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LENGTH: 235 amino acids
TYPE: amino acid
                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
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                          CRQFLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSM 120
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                                                                                 MDPARPLGLSILLLFLTEAALGDAAQEPTGNNAEICLLPLDYGPCRALLLRYYYDRYTQS
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CROFLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSM
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                                                                                                                                                                   100.0%; Score 1306; DB 22; ilarity 100.0%; Pred. No. 7.7e-138; Conservative 0; Mismatches 0;
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120
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Sequence 332, Application US/09466867
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 2010.1.478C2
CURRENT APPLICATION NUMBER: US/09/466,867
CURRENT FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 340
SOFTWARE: FASTSEQ for Windows Version 3.0
SECOND 332
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                                                                               US-09-466-867-332
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US-09-466-867-332
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SEQ ID NO 4
LENTH: 235
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Best Local Similarity
Matches 235; Conserva
                                   Query Match
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TITLE OF INVENTION: METHOD FOR TREATING RETINAL DEGENERATION
FILE REFERENCE: 0599-191P
CURRENT APPLICATION NUMBER: US/09/308,853
CURRENT FILING DATE: 1999-08-06
PRIOR APPLICATION NUMBER: PCT/JP98/04318
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 4
                                                                                              LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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  Conservative
                  100.0%; Score 1306; DB 24; 100.0%; Pred. No. 7.7e-138;
0,
  Mismatches
                                     DB 24;
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Sequence 332, Application US/09533077

GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Hangur, Chaitanya S.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
ITILE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C5
CURRENT APPLICATION NUMBER: US/09/533,077
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 800
SOPTMARE: FBSELSEQ for Windows Version 3.0
SEQ ID NO 332
                                                                                                                                                                                                                                                                       RESULT 11
US-09-533-077-332
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US-09-476-300-332
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US-09-476-300-332
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APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C3
CURRENT APPLICATION NUMBER: US/09/476,300
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 785
SOFTWARE: PASESEQ for Windows Version 3.0
SEQ ID NO 332
FORCER: 726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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TYPE: PRT
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APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Mannion, Jane
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR
FILE REFERENCE: 210121.478C6
CURRENT APPLICATION UNDER: US/09/546,259
CURRENT FILING DATE: 2000-04-10
NUMBER OF SEQ ID NOS: 803
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 332
LENGTH: 235
RESULT 13
US-09-560-406-332
IS-09-560-406-332
; Sequence 332, Application US/09560406
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
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; ORGANISM: Homo sapiens
US-09-533-077-332
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; ORGANISM: Homo sapiens
US-09-546-259-332
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US-09-546-259-332
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Pred. No. 7.7e-138;
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APPLICANT: PAIL LÍQUI

APPLICANT: PAIL LÍQUI

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.478C13

CURRENT APPLICATION NUMBER: US/09/677,419A

CURRENT FILING DATE: 2000-10-06

NUMBER OF SEQ ID NOS: 1825

SOFTWARE: PASCSEQ for Windows Version 3.0

SEQ ID NO 332

LENGTH: 235

TYPE: PRT

ORGANISM: Homo sapiens

US-09-677-419A-332
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APPLICANT: Lodes, Michael A.
APPLICANT: Vedvick, Tom
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C7
CURRENT APPLICATION NUMBER: US/09/560,406
CURRENT FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 824
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 332
LENGTH: 235
TYPER: PRT
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US-09-677-419A-332
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APPLICANT: Bangur, Chaitanya S
APPLICANT: Lodes, Michael J.
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc W.
                                                                   Matches
                                                                                                          Query Match
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Best Local Similarity
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ORGANISM: Homo sapiens
                                                               / Match 100.0%;
Local Similarity 100.0%;
hes 235; Conservative 0
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1 MDPARPIGISILILIFITEAALGDAAQEPTGNNAEICILFIDYGPCRALLIRYYYDRYTQS 60
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                                                               Score 1306; DB 26;
Pred. No. 7.7e-138;
D; Mismatches 0;
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; Sequence 1224, Application US/09760443
; GENERAL INFORMATION:
APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and J
FILE REFERENCE: BYZ12
CURRENT APPLICATION NUMBER: US/09/760,443
; CURRENT FILING DATE: 2001-01-16
Prior application data removed - refer to PALM or NUMBER OF SEQ ID NOS: 2164
; SOPTWARE: Patentin Ver. 2.0
; SEQ ID NO 1224
; LENGTH: 235
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; ORGANISM: Homo sapiens
US-09-760-443-1224
Search completed: March
Job time : 568 secs
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US-09-760-443-1224
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Best Local Similarity 100.0%;
Matches 235; Conservative 0
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Pred. No. 7.7e-138;
D; Mismatches 0;
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1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep:*

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US-11-287-121A-4
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PCT-US05-34335-39
PCT-US05-34335-39
PCT-US05-34335-11
US-11-287-121A-11
US-60-763-373-177
US-60-772-265-1
US-11-268-554-187
US-60-741-050-21
US-60-741-050-21
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US-11-107-643-1

US-11-107-643-2

US-11-107-643-3

PCT-US05-42298-1

PCT-US05-3435-54

US-11-302-208-1

US-11-302-208-1

US-11-302-208-1

PCT-US05-42298-1
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Sequence 332, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 4, Appli Sequence 4, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 11, Appli Sequence 117, Appli Sequence 177, Appli Sequence 21, Appli Sequence 24, Appli
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26
162.5	162.5	180	180	186	186	186	193.5	217.5	217.5	217.5	217.5	262	262	262	262	262	. 262	265	265
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Sequence 158,	Sequence 155,		Sequence 1411,	Sequence 19, A	Sequence 34, A	-	Sequence 1087,	Sequence 1027,	•		Sequence 118,	•	Sequence 27, A	•	Sequence 2, Appl	Sequence 1, Appl	Sequence 188,		•
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ALIGNMENTS

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APPLICANT: Fanger, Gary R.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Wedvick, Thomas S.

APPLICANT: Menabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C21
CURRENT FILING DATE: 2005-12-13
PRIOR APPLICATION NUMBER: US 10/283,017
PRIOR PILING DATE: 2002-10-28
PRIOR PILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: US 10/113,872
PRIOR APPLICATION NUMBER: US 10/017,754
PRIOR APPLICATION NUMBER: US 09/902,941
PRIOR PILING DATE: 2001-10-29
PRIOR PILING DATE: 2001-07-10
PRIOR PILING DATE: 2001-07-10
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US-11-301-554-332
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PRIOR FILING DATE: 2000-09-08
Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 2157
SOPTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 332
LENCTH: 235
TYPE: PRT
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OR FILING DATE: 2001-05-03
OR APPLICATION NUMBER: US 09/736,457
OR APPLICATION NUMBER: US 09/736,457
OR APPLICATION NUMBER: US 09/702,705
OR FILING DATE: 2000-10-30
OR PILING DATE: 2000-10-06
OR PILING DATE: 2000-10-06
OR PILING DATE: 2000-10-06
OR APPLICATION NUMBER: US 09/677,419
OR APPLICATION NUMBER: US 09/671,325
OR APPLICATION NUMBER: US 09/671,325
                                                                                                                                                                         FILING DATE: 2000-09-26
APPLICATION NUMBER: US 09/658,824
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Retter, Marc W.

Durham, Margarita
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APPLICANT: Kisiel, walter
APPLICANT: Chand, Hitendra
TITLE OF INVENTION: Human Kunitz-type Inhibitor with Enhanced Antifibrinolytic
TITLE OF INVENTION: Activity
FILE REFERENCE: 310.00170101
CURRENT APPLICATION NUMBER: US/11/107,643
CURRENT FILING DATE: 2005-04-15
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.2
SEQ ID NO 1
LENGTH: 213
TYPE: PRT
ORGANISM: homosapiens
US-11-107-643-1
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Sequence 2, Application US/11107643
GENERAL INFORMATION:
APPLICANT: Kisiel, Walter
APPLICANT: Chand, Hitendra
TITLE OF INVENTION: Auditz-type Inhibitor with Enhanced Antifibrinolytic
TITLE OF INVENTION: Activity
FILE REFERENCE: 310.00170101
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Matches 213;
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Best Local :
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100.0%; Pred. No. 7.2e-110;
tive 0; Mismatches 0;
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 LENGTH: 304
TYPE: PRT
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SEQUENCE 1, Application PC/TUS0542298
GENERAL INFORMATION:
APPLICANT: Dyax Corporation
ITILE OF INVENTION: PLASMIN-INHIBITORY THERAPIES
FILE REFERENCE: 10280-122W01
CURRENT APPLICATION NUMBER: PCT/US05/42298
CURRENT FILING DATE: 2005-11-22
PRIOR APPLICATION NUMBER: US 60/630,226
PRIOR APPLICATION NUMBER: US 60/630,226
PRIOR PILING DATE: 2004-11-22
NUMBER OF SEQ ID NOS: 24
SOPTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: artificial FARTURE: OTHER INFORMATION: mutated KD-1 US-11-107-643-3
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SOFTWARE: Patentin version 3.2
SEQ ID NO 3
LENGTH: 73
TYPE: PRT
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CURRENT FILING DATE: 2005-04-15
NUMBER OF SEQ ID NOS: 30
SOPTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 73
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Human Kunitz-type Inhibitor with Enhanced Antifibrinolytic TITLE OF INVENTION: Activity FILE REFERENCE: 310.00170101 CURRENT APPLICATION NUMBER: US/11/107,643 CURRENT FILING DATE: 2005-04-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kisiel, Walter APPLICANT: Chand, Hitendra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 98.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 DAAQEPTGNNAEICLLFLDYGFCRALLLRYYYDRYTQSCRQFLYGGCEGNANNFYTWEAC 82
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Pred. No. 7e-34;
1; Mismatches
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PCT-US05-34335-54
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PCT-US05-42298-1
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PCT-US05-34335-54
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Best Local Similarity
Matches 86; Conserv
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Best Local Similarity
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CURRENT APPLICATION NUMBER: PCT/US05/34335
CURRENT FILING DATE: 2005-09-22
PRIOR APPLICATION NUMBER: US 11/125,639
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APPLICANT: Beck, Thomas
APPLICANT: Ladner, Robert C.
TITLE OF INVENTION: KALLIKREIN INHIBITORS AND ANTI-THOMBOLYTIC AGENTS AND USES THEREC
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APPLICATION NUMBER: US 10/953,902
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                      GNDNNFVSREDCKRACAKAL---
                                                                                                                                                                                               CEGSTEKYPPNLSSMTCEKFPSGGCHRNRIENRFPDEATCMGPC------- 149
                                                                                                                                                                                                                                     ROCEEFIYGGCEGNQNRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLE---EDPGI 133
                                                                                                                                                                                                                                                                                                                            LLLNLAPAPLNADSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCKAIMKRFFFNIFT
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                                                                   NAVNNSLTPQSTKVPSLFEFHGPSWCLTPADRGLCRANENRFYYNSVIGKCRPFKYSGCG
                                                                                                           -----APKKI-----PSFCYSPKDEGLCSANVTRYYFNPRYRTCDAFTYTGCG 192
                                                                                                                                                    CRGYITRYFYNNQTKQCERFKYGGCLGNM--NNFETLEECKNICEDGPNGFQVDNYGTQL 191
29.7%;
llarity 30.3%;
Conservative 3:
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                                                                                                                                                                                                                                                                                                                                                                                                             37;
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                        -KKKKKMPKLRFA 224
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FITTLE OF INVENTION: PLASMIN-INHIBITORY THERAPIES
FILE REFERENCE: 10.80-122001
CURRENT APPLICATION NUMBER: US/11/267,121A
CURRENT FILING DATE: 2005-11-22
PRIOR APPLICATION NUMBER: US 60/630,226
PRIOR APPLICATION NUMBER: US 60/630,226
PRIOR FILING DATE: 2004-11-22
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 1
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; TYPE: PRT
; ORGANISM: Homo 8
US-11-287-121A-1
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US-11-302-208-1
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                                                            PRIOR APPLICATION NUMBER: US/10/753,068
PRIOR FILING DATE: 2004-01-08
PRIOR APPLICATION NUMBER: US 60/438,519
PRIOR FILING DATE: 2003-01-08
PRIOR PELLORIUS NUMBER: US 60/474,577
PRIOR PILING DATE: 2003-08-13
PRIOR PILING DATE: 2003-10-20
PRIOR APPLICATION NUMBER: US 60/509,260
PRIOR PILING DATE: 2003-10-08
PRIOR PILING DATE: 2003-10-08
PRIOR PILING DATE: 2003-10-20
PRIOR FILING DATE: 2003-10-20
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/11302208
GENERAL INFORMATION:
APPLICANT: Chen, Bao-Lu
APPLICANT: Huang, Chin-Yi
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Best Local Similarity
                                                                                                                                                                                                                                                                               APPLICANT: Huang, Chin-Yi
TITLE OF INVENTION: Stabilized Compositions Comprising Tissue Factor Pathway Inhibitor
TITLE OF INVENTION: Protein or Tissue Factor Pathway Inhibitor Variant Proteins
FILE REFERENCE: 12441.00054
CURRENT APPLICATION NUMBER: US/11/302,208
CURRENT FILING DATE: 2005-12-14
  NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
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APPLICANT: Ley, Arthur C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNENNFTSKQECLRACKKGFIQRISKGGLIKTKRKKKKQRVKIA 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.7%; Score 388; DB 7;
30.3%; Pred. No. 2.8e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76;
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US-11-337-518-1
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                                                                                                                                                     PRIOR APPLICATION NUMBER: US 09/973,211
PRIOR FILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-11-30
PRIOR PILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/473,668
PRIOR APPLICATION NUMBER: PCT/US96/09980
PRIOR FILING DATE: 1995-06-07
PRIOR PILING DATE: 1996-06-07
PRIOR PILING DATE: 1996-06-07
PRIOR PILING DATE: 1996-06-07
PRIOR PILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: US 09/973,211
PRIOR APPLICATION NUMBER: US 09/973,211
PRIOR APPLICATION NUMBER: US 09/443,099
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                                                                                              SOFTWARE: FastSEQ
SEQ ID NO 1
 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches 78; Conserv
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Formulation, Solubilization, Purification, and Refolding of TissuTITLE OF INVENTION: Pathway Inhibitor FILE REFERENCE: 012441.00013
                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                             PRIOR FILING DATE: 1999-11-18
                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/11/337,518
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                ORGANISM: Homo
                                                                TYPE: PRT
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                              LENGTH: 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89 ----IEKVPKVCRLQVSVDDQ--CEGSTEKYFFNLSSMTCEKFFSGGCHRNRIENRFPDE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 CLLPLDYGPCRALLLRYYYDRYTQSCRQFLYGGCEGNANNFYTWBACDDACWR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NVTRYYFNPRYRTCDAFTYTGCGGNDNNFVSREDCKRACAKAL------KKKKK 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dorin, Glenn J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KQRVKIA 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NENRFYYNSVIGKCRPFKYSGCGGNENNFTSKQECLRACKKGFIQRISKGGLIKTKRKRK 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EECKNI CEDGPNGFQVDNYGTQLNAVNNSLTPQSTKVPSLFEFHGPSWCLTPADRGLCRA
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Bild, Gary S.
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Tsang, Michael
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Hora, Maninder S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen, Bao-lu
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                                              sapiens
                                                                                                             for Windows
                                                                                                                                                                                                                                                                                                                                                                                                                     Gary V.
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29.4%;
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                                                                                                             Version 4.0
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Score 384.5;
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7;
Length 276;
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Sequence 4, Application PC/TUSO542298
GENERAL INFORMATION:
APPLICANT: Dyax Corporation
TITLE OF INVENTION: PLASMIN-INHIBITORY THERAPIES
FILE REFERENCE: 10280-122W01
CURRENT APPLICATION NUMBER: PCT/USO5/42298
CURRENT FILING DATE: 2005-11-22
PRIOR APPLICATION NUMBER: US 60/630,226
PRIOR FILING DATE: 2004-11-22
INUMBER: FASE ID NOS: 24
SOFTWARE: FASE SEQ ID NO 4
LENGTH: 58
TYPE: DET
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APPLICANT: Blair, Henry
APPLICANT: Beck, Thomas
APPLICANT: Ladner, Robert C.
APPLICANT: Ladner, Robert C.
TITLE OF INVENTION: KALLIKREIN INHIBITORS AND ANTI-THOMBOLYTIC AGENTS AND USES THEREOI FILE REFERENCE: 10280-131W01
CURRENT APPLICATION NUMBER: PCT/US05/34335
CURRENT FILING DATE: 2005-09-22
PRIOR APPLICATION NUMBER: US 11/125,639
PRIOR APPLICATION NUMBER: US 10/953,902
PRIOR FILING DATE: 2005-09-27
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 37
LENGTH: 58
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 37, Application PC/TUS0534335 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KTTLQQEKPDFCFLE---EDFGICRGYITRYFYNNQTKQCERFKYGGCLGNM--NNFETL 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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; Pred. No. 1.2e-26;
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PCT-US05-34335-37

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Synthetically generated peptide

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APPLICANT: Devy, Laetitia
APPLICANT: Ley, Arthur C.
APPLICANT: Ledher, Robert C.
TITLE OF INVENTION: PLASMIN-INHIBITORY THERAPIES
FILE REFERENCE: 10280-122001
CURRENT APPLICATION NUMBER: US/11/287,121A
CURRENT FILING DATE: 2005-11-22
PRIOR APPLICATION NUMBER: US 60/630,226
PRIOR FILING DATE: 2004-11-22
NUMBER OF SEQ ID NOS: 24
SOPTWARE: PASCECQ for Windows Version 4.0
SEQ ID NO 4
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                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/630,226
PRIOR FILING DATE: 2004-11-22
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 61
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Best Local &
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Application PC/TUS0542298 GENERAL INFORMATION:
                                      Matches
                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -11-287-121A-4
                                                                                                                                                                                                                                                                                                                          APPLICANT: Dyax Corporation
TITLE OF INVENTION: PLASMIN-INHIBITORY THERAPIES
FILE REPERENCE: 10280-122001
CURRENT APPLICATION NUMBER: PCT/US05/42298
CURRENT FILING DATE: 2005-11-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEATURE: OTHER INFORMATION: Synthetically generated peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                      FEATURE:
                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                 OTHER INFORMATION: Synthetically generated peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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les 58; Conserv
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                                      61;
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92 VPKVCRLQVSVDDQCEGSTEKYFFNLSSMTCEKFFSGGCHRNRIENRFPDEATCMGFCAP 151
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100.0%; Pred. No. 1.2
Live 0; Mismatches
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                                                      Score 342; DB 1; Pred. No. 1.6e-26;
                                      Mismatches
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Sequence 38, App...
; Sequence 38, App...
; GEMERAL INFORMATION:
; APPLICANT: Blair, Henry
; APPLICANT: Beck, Thomas
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PCT-US05-34335-38
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                                                                           ; OTHER INFORMATION: Synthetically generated peptide
US-11-287-121A-16
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                    Best
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16, Application US/11287121A GENERAL INFORMATION:
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Best Local
                                         Query Match
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PRIOR TILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 10/953,902
PRIOR FILING DATE: 2004-09-27
NUMBER OF SEQ ID NOS: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 10280-131W01
CURRENT APPLICATION NUMBER: PCT/US05/34335
CURRENT FILING DATE: 2005-09-22
                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/11/287,121A
CURRENT FILING DATE: 2005-11-22
PRIOR APPLICATION NUMBER: US 60/630,226
PRIOR FILING DATE: 2004-11-22
                                                                                                                                                                                                                                                                                                           APPLICANT: Devy, Laetitia
APPLICANT: Ley, Arthur C.
APPLICANT: Ladner, Robert C.
TITLE OF INVENTION: PLASMIN-INHIBITORY THERAPIES
FILE REFERENCE: 10280-122001
                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ladner, Robert C.
TITLE OF INVENTION: KALLIKREIN INHIBITORS AND ANTI-THOMBOLYTIC AGENTS AND USES THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Synthetically generated peptide
                                                                                                             ORGANISM: Artificial Sequence FEATURE:
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TYPE: PRT
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     26.2%; Score 342; DB 7; 1
100.0%; Pred. No. 1.6e-26;
rive 0; Mismatches 0;
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; Pred. No. 1.6e-26;
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Job time : 40 Becs	Search completed: March 9, 2006, 20.08.42	61 K 61	152 K 152	1 VPKVCRLQVSVDDQCEGSTEKYFFNLSSMTCEKFFSGGCHRNRIENRFPDEATCWGFCAP 60	92 VPKVCRLQVSVDDQCEGSTEKYFFNLSSMTCEKFFSGGCHRNRIENRFPDEATCMGFCAP 151

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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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        E34398 Vascular sm
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I14875 Sequence 1
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L27624 Homo sapien
EC005330 Homo sapien
EC0412591 Sequence
CQ717511 Sequence
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CQ717518 Sequence
CQ717518 Sequence
CX91946 Homo sapien
CX98142 Sequence
CX9992 Homo sapien
CX981788 Sequence
CX9992 Homo sapien
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CX918142 Sequence
CX9992 Homo sapien
CX98144 Sequence
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ALIGNMENTS

ore 979; DB 6; Length 979; red. No. 1.6e-216; Mismatches 0; Indels
Location/Qualifiers (39)(743).
C12Q1/68, A61K37/64,A61K37/02,C12N15/00
YOSHIKI YUI A61K38/55,A61K31/00,A61K31/00,A61K38/00,C07K14/47,C12N15/09,
Vascular smooth muscle proliferator Patent: JF 2000128802-A 1 09-MAY-2000; SHTONOGT & CO LTD
/
Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini;
979 bp DNA proliferator.

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1 GGACGCCTTGCCCAGCGGGCCCCGACCCCCTGCACCATGGACCCCGCTCGCCCCCTGG 60

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Patent: JP 2000128803-A 1 09-MAY-2000;
SHIONOGI & CO LTD
OS Homo sapiens (human)
PN JP 2000128803-A/1
PD 09-MAY-2000
PF 19-OCT-1998 JP 1998296759
PR YOSHIKI YUI
PC C12M15/09,
PC C12M15/09,
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 979)
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JP 2000128803-A/1.
                                                                                                                  GGTCCACAGAAAAGTATTTCTTTAATCTAAGTTCCATGACATGTGAAAAAATTCTTTTCCG
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CTGCCAATGTGACTCGCTATTATTTTAATCCAAGATACAGAACCTGTGATGCTTTCACCT
                                                               TCTGCGCACCAAAGAAAATTCCATCATTTTGCTACAGTCCAAAAGATGAGGGACTGTGCT
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A61K39/395,A61K39/395,A61K31/00,A61K31/00,C07K16/36,C12N5/10,
C12N15/09,
C12P21/02,G01N33/50,G01N33/53//(C12P21/02,C12R1:91),C12N5/00,
C12N15/00
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(39)..(743).
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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1 (bases 1 to 979)

Sprecher, C.A., Kisiel, W. a
DNA encoding Aswel human k
relating thereto
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Sequence 1
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                                  CAACAGGAAATAACGCGGAGATCTGTCTCCTGCCCCTAGACTACGGACCCTGCCGGGCCC
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Location/Qualifiers
                                                                                                                                                                                        organism-"unknown"
mol_type="unassigned
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from patent US 5455338
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          Unclassified.

1 (bases / to 979)
Sprecher C.A., Kisiel W. and Foster, D.C.
Inhibit/on of blood coagulation by human-kunitz-type inhibitors
Patent / US 5728674-A / 17-MRR-1998;
LUS 572807-A / 17-MRR-1998;
LUS 572807-A / 17-MRR-1998;
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/organiem="unknown"
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Sequence 1:
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       moI_type="unassigned DNA"
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from patent US 5728674.
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Best Local Similarity 100.0%; Pred. No. 1.6e-216;
Matches 979; Conservative 0; Mismatches 0;
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                                                                        GTGCAAAAGCTTTGAAAAAGAAAAAAGAAGATGCCAAAGCTTCGCTTTGCCAGTAGAATCC
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Unclassified.

1 (bases 1 to 979)

1 (bases 1 to 979)

Au-Young, J. and Seilhamer, J.J.

Composition for the detection of signaling |
Patent: US 6500938-A 1378 31-DEC-2002;
Incyte Genomics, Inc.; Palo Alto, CA;
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Sequence 13'
AR270815
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GTGCAAAAGCTTTGAAAAAGAAAAAAGAAGATGCCAAAGCTTCGCTTTGCCAGTAGAATCC
                             CTGCCAATGTGACTCGCTATTATTTAATCCAAGATACAGAACCTGTGATGCTTTCACCT
                                                                                       GGTCCACAGAAAAGTATTTCTTTAATCTAAGTTCCATGACATGTGAAAAAATTCTTTTCCG
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llarity 100.0%;
Conservative 0;
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/mol_type="genomic
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Pred. No. 1.6e-216;
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Sprecher,C.A., Kislel,W. and Foster,D.C.
Antibodies to human kunitz-type inhibitor
Patent: 05 656746-A 1 02-DEC-2003;
ZymoGenet(cs, Inc.) and University of New 1
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AR437163.1 GI:40200260
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/mol_type="genomic DNA"
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Homo sapiens
Sukaryota; Metazoa; (
Mammalia; Eutheria; I
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Homo sapiens tissue factor pathway
127624
127624.1 GI:441149
tissue factor pathway inhibitor-2.
Homo sapiens /hwm--
                                                                                                                                          1 (bases 1 to 979)
Sprecher, C.A., Kislel, W., Mathewes, S. and Foster, D.C.
Molecular cloning, expression, and partial characterization
second human tissue-factor-pathway inhibitor
Proc. Natl. Acad. Sci. U.S.A. 91 (8), 3353-3357 (1994)
                                                                                                          Original source text: Homo sapiens
                                                                                                                                                                                                   Hominidae; Homo.
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                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
39...746
 /note="putative"
/codon_start=1
/product="tissue factor pathway inhibitor-2"
/protein ide"AAAA20094.1"
/db_xref="GI:441150"
                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini;
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inhibitor-2 mRNA,
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TTTATATAACTAGCTGCTATTCAAATGTGAGTCTACCATTTTTAATTTATGGTTCAAC
                                                                                                                GCTTATTTGCCTTTATGGTTGTATCTGAAGAATAATATGACAGCATGAGGAAACAAATCA 840
                                                                                                                                                                                                                          GTGCAAAAGCTTTGAAAAAGAAAAAAGATGCCAAAGCTTCGCTTTGCCAGTAGAATCC
                                                                                                                                                                                                                                                                          ATACTGGCTGTGGAGGGAATGACAATAACTTTGTTAGCAGGGAGGATTGCAAACGTGCAT
                                                                                                                                                                                                                                                                                                                           CTGCCAATGTGACTCGCTATTATTTTAATCCAAGATACAGAACCTGTGATGCTTTCACCT
                                                                                                                                                                                                                                                                                                                                                                                 TCTGCGCACCAAAGAAAATTCCCATCATTTTGCTACAGTCCAAAAGATGAGGGACTGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGGGTGTCACCGGAACCGGATTGAGAACAGGTTTCCAGATGAAGCTACTTGTATGGGCT
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                                                           TTGGTGATTTATTCACCAGTTTTTATTAATACAAGTCACTTTTTCAAAAAATTTGGATTTT
                                                                                                                                                                         GGAAAATTCGGAAGAAGCAATTTTAAACATTCTTAATATGTCATCTTGTTTTGTCTTTATG
                                                                                                                                                                                                      GTGCAAAAGCTTTGAAAAAGAAAAAGAAGATGCCAAAGCTTCGCTTTGCCAGTAGAATCC
                                                                                                                                                                                                                                                                                                                                                                                                                     GTGGGTGTCACCGGAACCGGATTGAGAACAGGTTTCCAGATGAAGCTACTTGTATGGGCT
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                                                                                                                                                                                                                                                        ATACTGGCTGTGGAGGAATGACAATAACTTTGTTAGCAGGAGGATTGCAAACGTGCAT
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llarity 100.0%;
Conservative
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CRALLLRYYYDRYTQSCRQPLYGGCEGKNANFYTWAELGNDACHRIEKVEKVCRLQVSV
DDQCEGSTEKYFPNLSGWTCEKEPSGGCHNNIETNFPDEATCMGFCAPKKIBEFCS
PKDEGLCSANVTRYYFNPRYRTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKM
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Pred. No. 1.6e-216;
; Mismatches 0;
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JOURNAL
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AUTHORS
CONSRIM
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COMMENT
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Et 1 (Dases 1 to 1203)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsleh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuk, S.,

Carninci, F., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosāk, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Mammalian Gene Collection program Team

Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     961
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Homo sapiens tissue factor pathway inhibitor 2, mRNA (cDNA clone
MGC:12416 IMAGE:3929933), complete cds.
BC005330
                                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLIL at: http://image.llnl.gov Series: IRAL Plate: 16 Row: j Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 31543803.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (27-MAR-2001) National Institutes of Health, Gene Collection (MGC), Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94:
                                                                                                                                                                                                                                                                                                                                                                                                                           Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human and mouse CDNA sequences
human and mouse CDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/db_xref="taxon:9606"
                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                              http://www-shgc.stanford.edu
(Dickson, Mark) mcd@paxil.stanford.edu
M., Schmutz, J., Grimwood, J., Rodriquez,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Metazoa;
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ORIGIN
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Best Local Similarity
Matches 979; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGACGCCTTGCCCAGCGGGCCGCCCGACCCCTGCACCATGGACCCCGCTCGCCCCTGG
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                                                                                                                                                            GTGGGTGTCACCGGAACCGGATTGAGAACAGGTTTCCAGATGAAGCTACTTGTATGGGCT
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                                                                                                           TCTGCGCACCAAAGAAATTCCATCATTTTGCTACAGTCCAAAAAGATGAGGGACTGTGCT
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llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="TFPI2"
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/tissue type="Brain, primitive no
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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Pred. No. 1.6e-216;
0; Mismatches 0;
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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CQ412591
CQ412591.1 GI:-
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Genes, compositions, kits, and mathod for identification,
Genes, composition, and therapy of ovarian cancer
Patent: WO 0170979-A 19662 27-SEP-2001;
Millennium Pharmaceuticals Inc. (US)
Location/Qualifiers
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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                                                                                               TTTATATATACTAGCTGCTATTCAAATGTGAGTCTACCATTTTTAATTTATGGTTCAAC
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                                              TGTTTGTGAGACTGAATTC
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Patent: WO 02068579-A 3445 06-SEP-2002,
PE Corporation (NY) (US)
                                                                   Venter, C.J., Adams, M.C., Li, P.W. and Myers, B.W. Kits, such as nucleic acid arrays, comprising a majority humanexons or transcripts, for detecting expression and o
                                                                                                                  Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaila; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Sequence 3445 from Patent WO02068579.
CQ717511 GI:42278368
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                    Location/Qualifiers
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  /organism="Homo sapiens"
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TGTTTGTGAGACTGAATTC
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Pred. No. 3.7e-216;
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NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.
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AK129833.1 GI:34526454
Oligo capping; fis (full insert sequence).
Homo sapiens (human)
Homo sapiens
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Sugano, S. and Suzuki, Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AK129833 2206 bp mRNA linear PRI 10-SEP-2003 AK129833 classifier to sapiens cDNA FLJ26323 fis, clone HRT00813, highly similar to Tissue factor pathway inhibitor 2 precursor (TPPI-2).
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/mol_type="mRNA"
/db xref="taxon:9606"
/clone="HRT00813"
/tlssue type="heart"
/clone_Tib="HRT"
/note="cloning vector: pwg
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                                                                                                                                                                                                                                                                                                                                                                 Score 977.4; DB
Pred. No. 3.8e-21
0; Mismatches
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3.8e-216;
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                                                         Hominidae; Homo.

1 (bases 1 to 1055)

Xu,Y., Li,T. and Du,G.

Direct Submission

Submitted (21-JUL-2004) Department of Molecular Biology, Medical Research Center, Shenzhen People's Hospital, Medical School of Jinan University, Dongmen North Road 1017, Shenzhen, Guangdong 518020, P.R. China
                                                                                                                                                                                                                                                                                                             Homo sapiens tissue factor pathway complete cds. AY691946
                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/organism="Homo sapiens"
/mol_type="mRNA"
                                                   Location/Qualifiers
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/td_xref="GI:51475144"
/td_xref="GI:514751444"
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PKLRFASRIRKIRKKQF"
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Pred. No. 8.7e-216;
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CQ981542.1 G
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Hinzmann, Bernd (DE); Germann, Klaus (DE); Heiden, Rosenthal, Andre (DE)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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                       GGTCCACAGAAAAGTATTTCTTTAATCTAAGTTCCATGACATGTGAAAAAATTCTTTTCCG
                                                                                                        TACTTCTCCGTTACTACTACGACAGGTACACGCAGAGCTGCCGCCAGTTCCTGTACGGGG
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Query Matches Matches Qy Db	PEATURES BOUTC ORIGIN	REFERENCE AUTHORS TITLE JOURNAL	SOURCE	RESULT 14 CS091788 LOCUS DEFINITION ACCESSION VERSION VERSION	p &	B &	₽ &	8 8	B 8	B 8	<u> </u>	<u> </u>	₽ &	₽ &
Query Match 99.3%; Score 972.2; DB 6; Length 1142; Best Local Similarity 99.7%; Pred. No. 6e-215; Matches 974; Conservative 0; Mismatches 3; Indels 0; Gaps 0; Matches 974; Conservative 0; Mismatches 3; Indels 0; Gaps 0; 1 GGACGCCTTGCCCAGCGGGCCCCGACCCCCTGCACCATGGACCCCGCTCGCCCCCTGG 60	O	Hominidae; Homo. 1 Kochan, J. P. and Rogr Specific markers for Patent: EP 1533619-Patent. EP 1633619-Patent.	Homo sapier Homo sapier Eukaryota; Mammalia; I	CS091788 N Sequence 23 from Patent EP1533619. CS091788 CS091788.1 GI:66949353	961 TGTTTGTGAGACTGAAT 977 979 TGTTTGTGAGACGAATT 995	901 TITATATATAACTAGCTGCTATTCAAATGTGAGTCTACCATTTTTAATTTATGGTTCAAC 960 	841 TTGGTGATTTATTCACCAGTTTTTATTAATACAAGTCACTTTTTCAAAAATTTTGGATTTT 900	781 GCTTATTTGCCTTTATGGTTGTATCTGAAGAATAATATGACAGCATGAGGAAACAAATCA 840 	721 GGAAAATTCGGAAGAAGCAATTTTAAACATTCTTAATATGTCATCTTGTTTGT	661 GTGCAAAAGCTTTGAAAAAGAAAAAGAAGATGCCAAAGCTTCGCTTTGCCAGTAGAATCC 720 	601 ATACTGGCTGTGGAGGGAATGACAATAACTTTGTTAGCAGGGAGGATTGCAAACGTGCAT 660	541 CTGCCAATGTGACTCGCTATTATTTTAATCCAAGATACAGAACCTGTGATGCTTTCACCT 600	481 TCTGCGCACCAAAGAAAATTCCATCATTTTGCTACAGTCCAAAAGATGAGGGACTGTGCT 540	421 GTGGGTGTCACCGGAACCGGATTGAGAACAGGTTTCCAGATGAAGCTACTTGTATGGGCT 480
RESULT 15 HUMPP5 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	QY QY	& & &	gb Qy	D Qy	ଷ ନ୍ଧ ଷ	D Qy	B &	B &	B &	B 8	B &	B 8	B 8	 B &
HUMPP5 Homo sapiens mR D29992 D29992.1 GI:48 PP5; placental	919 961 979													

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Miyagi,Y.
Miyagi,Y.
Direct Submission
Submitted (25-APR-1994) Yohei Miyagi, Yokohama City University
School of Medicine, Dept. of Pathology, Fukuura 3-9, Kanazawa-ku,
Yokohama, Kanagawa 236, Japan (Tel:045-787-2587, Pax:045-786-0191)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Miyagi,Y., Koshikawa,N., Yasumitsu,H., Miyagi,B., Hirahara,F., Aoki,I., Misugi,K., Umeda,M. and Miyazaki,K. CDNA cloning and mRNA expression of a serine proteinase inhibitor secreted by cancer cells: identification as placental protein 5 and tissue factor pathway inhibitor-2 J. Biochem. 116 (5), 939-942 (1994)
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Search completed: March 11, 2006, 07:00:31 Job time : 5420 secs

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Copyright (c) 1993 - 2006 Biocceleration Ltd.

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Maximum Match 100%
Listing first 45 summaries
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Ad156576 Human pol
Abv94764 Human pan
Ad145772 Human cDN
Ad45369 Human cDN
Ad45337 Human cDN
Ad45337 Human cis
Abs76528 Lung canc
Abx76528 Lung canc
Abx08764 Angiogene
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3			Location/Qualifiers 39746 /*tag= a		otease-	protease-inhibitor	~		979 BP	2		9 ACH22862		0 ACH35990	_	12 ADE			B ACA10386						8 ABZ20248						
			ere		Kunitz-type inhibitor; protease-inhibitor; enzyme anticoagulant; deep vein thrombosis; TPPI-2; ds.	itor TFPI-2 DNA.				ALIGNMENTS	5236	2862	9890	5990	2027	ADB72120	45583	9337	0386	8146	2778	910	0205	0259	0248	221	0262	6079	0218	ABZ20345	*3636
					enzyme-inhibitor; 2; ds.						Ach352:	Ach22862	Ad139890	Ach35990	ALJ19502	Ade723	Adh45	Abx99337 I	Aca103	Aaf68146	Ach3277	Ach36910	Abz202	Abz20259	Abz20248	AAV86987	Abz2026	Aas06079	Abz20218	Abz20345	Advasana Advasana
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CCX8X99X55X73X8X8X
                                                 WPI; 1995-193821/25.
P-PSDB; AAR74977.
                                                                    Sprecher CA,
                                                                                 (ZYMO) ZYMOGENETICS INC. (UYNE-) UNIV NEW MEXICO STATE.
                                                                                                     05-NOV-1993;
                                                                    Kisiel W,
                                                                                                     93US-00147710.
                                                                     Foster DC;
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This DNA sequence allows for the production of human recombinant Kunitz-type protease-inhibitor in large quantities that may be readily purified

Human Kunitz-type protease inhibitors - treatment of deep vein thrombosis.

used as anticoagulants and in the

Claim 4; Page 48; 65pp; English.

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                                                                                           The invention relates to a combination which, comprises a number of CC polynucleotide probes comprising a sequence selected from one of the 1490 CC sequences mentioned in the specification. The combination is useful as an CC array element in a microarray for monitoring the expression of a number CC of target polynucleotides. The microarray is particularly useful in the CC diagnosis and treatment of cancer and immunopathology and neuropathology. The microarray is useful in diagnostics and treatment regimens, drug CC discovery and development, toxicological and carcinogenicity studies, CC forensics and pharmacogenomics. The microarray is also useful for CC monitoring progression of diseases and for developing sophisticated profiles for the effects of currently available therapeutic drugs. The CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs and genomic fragments and in research and diagnostic applications. The CC carray can detect changes in expression in a large number of genes coding for different signaling pathway populations which can be used to diagnose CC various diseases including cancer e.g. adenocarcinoma and leukaemia, CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease and For diagnose of the invention. Note: The sequence tapsesents a polynucleotide CC probe of the invention. Note: The sequence data for this patent did not commat directly from USPTO at the Invention of the printed specification but was obtained in electronic command the converse commence the Interconverse co
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GACGCCTTGCCCAGGGGCCCCCCGACCCCCTGCACCATGAACCCCGCTCGCCCCCTGG

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GGCTGTCGATTCTGCTGCTTTTCCTGACGGAGGCTGCACTGGGCGATGCTGCTCAGGAGC

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GGACGCCTTGCCCAGCGGGCCGCCCGACCCCCTGCACCATGGACCCCGCTCGCCCCCTGG

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The invention relates to a composition of polynucleotide probes
CC comprising first polynucleotide probes comprising at least a portion of a
CC gene encoding a receptor-like polypeptide, second polynucleotide probes
CC comprising at least a portion of a gene encoding a transducing
CC of a gene encoding an effector-like polypeptide. The probes of the
CC composition are useful as array elements in a microarray for monitoring
CC diagnosis and treatment of cancer, an immunopathology or a
CC diagnosis and carcinogenicity studies, forensics or pharmacogenomics.
CC Microarrays can also be used for drug discovery and development,
CC Microarrays can also be used for monitoring the propession of diseases
CC Microarrays can also be used for monitoring the progression of diseases
CC microarray can also be used for monitoring the progression of diseases
CC microarray can also be used for monitoring the progression of diseases
CC microarray can also be used for monitoring the progression of diseases
CC microarray can also be used to purify a subpopulation
CC of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile
CC is also useful for the diagnosis and treatment of cancer, e.g. cancers of
CC the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,
CC an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or
CC ulcerative colitis, or a neuropathology, e.g. dementia, ammesia,
CC epilepsy, Alzheimer's disease or depression. This sequence represents a
CC bhained in electronic format directly from USPTO at
CC obtained in electronic format directly from USPTO at
                                                                                   Matches
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New composition comprising polynucleotide probes, useful as array elements in a microarray for monitoring the expression of target polynucleotides or purifying a subpopulation of mRNAs, cDNA, or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; probe; ss; receptor-like polypeptide; transducing polypeptide; effector-like polypeptide; cancer; immunopathology; neuropathology; drug development; toxicology; carcinogenicity; signalling pathway polypeptide; adrenal gland; bladder; bone; bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS; diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology; dementia; amnesia; epilepsy; Alzheimer's disease; depression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; SEQ ID NO 1378; 73pp; English
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                    n 100.0%; Score 979; DB 12; Similarity 100.0%; Pred. No. 1.3e-257;
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Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
                      Human pancreatic cancer expressed cDNA SEQ ID NO 145.
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CAACAGGAAATAACGCGGAAGATCTGTCTCCTGCCCCTAGACTACGGACCCTGCCGGGCCC

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GGACGCCTTGCCCAGCGGGGCCCCCGACCCCCTGCACCCATGGACCCCCGCTCGCCCCCCTGG

GANCGCCTTGCCCAGCGGGCCGGCCCGACCCCCTGCACCATGGACCCCGCTCGCCCCCTGG GGCTGTCGATTCTGCTGCTTTTTCCTGACGGAGGCTGCACTGGGGCGATGCTGCTCAGGAGC

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Query Match
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21-MAR-2001;
28-APR-2001;
16-MAY-2001;
                                                                                in a patient and compositions comprising polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations and antigen presenting cells expressing the polypeptide are useful in treating pancreatic cancer and stimulating an immune response. The polynucleotides can be used as probes or primers for nucleic acid hybridisation, in the design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in the tumour cells, in vaccines and for gene therapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                               The invention relates to an isolated polynucleotide (I) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b) complements of (a); (c) sequences consisting of at least 20 contiguous residues of (a); (d) sequences that hybridize to (a), under moderately stringent conditions; (e) sequences having at least 75% or 90% identity to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
                                                 Sequence 1172 BP; 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and pancreatic tumor diagnosing, preventing and/or treating cancer, pa
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31-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 145; 300pp + Sequence Listing; English
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20-AUG-2001;
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100.0%; Score 979; DB 6; Similarity 100.0%; Pred. No. 1.4e-257;
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2001US-027851P.
2001US-0287112P.
2001US-0291631P.
2001US-0305484P.
2001US-0313999P.
2001US-031399P.
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Matches Query Match Best Local (

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The invention relates to nucleic acid markers which are overexpressed in covarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides concerned by the markers, antibodies that selectively bind to the corresponding to a marker of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer invention and a method of treating a patient at risk control normal (i.e. non-covarian cancer inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense ollgomucleotide complementary to a marker of the cinvention. The markers are useful for assessing if a patient is afflicted with ovarian cancer sample. A difference between the capression levels indicates ovarian cancer: The level of expression of the marker in a control non-ovarian cancer sample. A difference between the capression levels indicates ovarian cancer: The level of expression of a marker in a control non-ovarian cancer: The level of expression of a capression of the marker in a control non-ovarian cancer. The presence of protein or protein cappending to the marker. The presence of protein or protein cappending to the marker. The presence of protein or protein cappending to the marker. The presence of protein or protein cappending to the marker. The presence of a transcribed cappending to the marker. Alternatively, the level of expression of the marker in a portion of the marker is also used for monitoring the marker, under stringent conditions. The patient which involves detecting expression. The method at a subsequent time and comparian tissue sample. A composition comprising a marker in a patient conversion the expression. The method at a subsequent conversion the involves detecting expression. The method at a subsequent conversion to the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DN
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25-MAY-2000; 2000US-0201124P.
15-JUN-2000; 2000US-0211940P.
07-JUL-2000; 2000US-0216820P.
25-JUL-2000; 2000US-0220661P.
21-DEC-2000; 2000US-0257672P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
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This invention relates to a combination comprising several cDNAs that are differentially expressed in activated vascular tissue. The invention also colored conditions as high throughput method for detecting differentially expressed conditions in a sample. The cDNAs of the invention may have antiarteriosclerotic; cytostatic; cardiant, hypotensive; antidiabetic; cymaecological; vasotropic and cerebroprotective activities and may be used in gene therapy. The cDNAs of the invention may be used in a high-condition and the condition of the invention may be used in a high-condition. A protein encoded by the cDNA may be used in a high-condition and protein encoded by the cDNA may be used to screen several molecules or compounds to identify a ligand that specifically binds a cDNA of the condition of the used to detect a protein in a sample or purify a natural or compound; the condition of the protein that can be used to detect a protein in a sample or purify a natural or conditions to injury, restension, diabetes, pre-clampsia, isohaemia-reperfusion conditions, treating, or monitoring the progression of treatment conditions, hypertension, diabetes, pre-cclampsia, isohaemia-reperfusion conditions, the protein also be used for large-scale genetic or gene expression analysis of several new mucleic acid conditions pre-pathologic disorders, and chronic or acute disease genetic or gene expression analysis of several new mucleic acid conditions pre-pathologic disorders, and chronic or acute disease genetic or gene expression analysis of several new mucleic acid conditions pre-pathologic disorders, and chronic or acute diseases conditions are proteins and conditions of the protein acid molecules for this patent sequence represents a cDNA of the invention conditions of the protein conditions of the condition, but the condition of the protein conditions of the protein conditio
Combination for diagnosing, staging, treating, or monitoring the progression of treatment of a vascular disease, e.g. atherosclerosis, comprises several cDNAs that are differentially expressed in activated
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08-JAN-2001;
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Sequence 2540 BP; 806 A; 458 C; 534 G; 742 T; 0 U; 0 Other;

Query Match Best Local 9

Similarity

100.0%;

Score 979; DB 8; Pred. No. 2e-257;

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                                                          TACTTCTCCGTTACTACGACAGGTACACGCAGAGCTGCCGCCAGTTCCTGTACGGGG
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                                        TACTTCTCCGTTACTACTACGACAGGTACACGCAGAGCTGCCGCCAGTTCCTGTACGGGG
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                                                                                                          human; differential expression; transactivator; proto-oncogene; neuroblastoma; small cell lung cancer; cytostatic; gene therapy
                                                                          Homo sapiens
                                                                                                                                           Human cDNA differentially expressed in MYCN activated cells SeqID 143
                                                                                                                                                                 06-MAY-2004 (first entry
                                                                                                                                                                                                             ADJ56337 standard; cDNA; 2540
          25-FEB-2002; 2002US-00084817
                                                      US2003119009-A1
                                                                                               oblastoma; small activated cell.
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(STUA/) STUART S G.
(NUCH/) NUCHTERN J G
(PLON/) PLON S B.
(SHOH/) SHOHET J M.
                                                                                                                                                                          New genes regulated by MYCN activation, useful in gene therapy, particularly for treating a subject with e.g. neuroblastoma or other cancers, or for diagnosing, staging or monitoring the treatment of the
                                                                                                                                                   Claim 1; SEQ ID NO 143; 27pp; English
                                                                                                                                                                                                          WPI;
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This invention relates to novel isolated cDNAs that are differentially expressed in MYCN activated cells. Specifically, it refers to polynucleotide sequences that exhibit differential expression patterns in cells activated by the transactivator MYCN, where MYCN is a protoconcogene that is amplified in neuroblastoma cells and is common in small cell lung cancers. The present invention describes these cDNA molecules as useful for in hybridisation assays to detect expression of nucleic acids for complementary nucleic acids) in a present in a given sample, as well as for screening assays by identifying molecules or compounds that specifically bind the cDNA as a light toytostatic activity and can also be used for gene therapy purposes. This polynucleotide sequence is a cDNA that is differentially expressed in MYCN activated cells, given in an the printed specification but has been obtained in electronic format from the US Patent Office at ftp.seqdata.uspto.gov/sequence.html?DocID=20030119009.

Sequence 2540 BP; 806 A; 458 C; 534 G; 742 T; 0 U; 0 Other;

Query Match 100 Best Local Similarity 100 Matches 979; Conservative 100.0%; Score 979; DB 10; 100.0%; Pred. No. 2e-257; tive 0; Mismatches 0; Length 2540; Indels ç

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                              GGTCCACAGAAAAGTATTTCTTTAATCTAAGTTCCATGACATGTGAAAAATTCTTTTCCG
                                                                                              TACTTCTCCGTTACTACTACGACAGGTACACGCAGAGCTGCCGCCAGTTCCTGTACGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mesenchymal stem cell; marker gene; serine protease inhibitor; cysteine protease inhibitor; adrenomedullin; apolipoprotein D; collagen type XV alpha 1; CUG triplet repeat RNA binding protein; dermatopontin; isocitrate dehydrogenase 2; major histocompatibility complex class II; MHC class II; DR beta 3; DR alpha; protein tyrosine kinase 7; Sam68-like phosphotyrosine protein; C-type lectin superfamily member 2; matrix metalloprotease 1; cells electin superfamily member 2; microarray; DNA chip; detection; tissue factor pathway inhibitor 2; microarray; DNA chip; detection;
     Kato
                                                                                                                                                                                                                            27-FEB-2004;
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                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                 (NISC-) JAPAN SCI
(TWOC-) TWO CELLS
(KATO/) KATO Y.
                                                                                                                                                                     10-MAR-2003; 2003JP-00063077.
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DR GENBANK; AL550357.

EX XX

New gene markers e.g. serine or cysteine protease inhibitor gene, major PT histocompatibility complex class II gene specific for mesenchymal stem cells, useful for detecting and identifying mesenchymal stem cells. SEQ ID NO 19; 171pp; Japanese.

XX

Claim 1; SEQ ID NO 19; 171pp; Japanese.

XX

The invention relates to marker genes for detecting mesenchymal stem cells. Selected from approximately 145 genes. The mesenchymal stem cell CC marker genes include the serine (or cysteine) protease inhibitor gene (C (ADS19160), the adrenomedullin gene (ADS19161), the apolipoprotein D gene (C (ADS19163), the collagen type XV alpha 1 gene (ADS19165), the CUG triplet CC repeat RNA binding protein 2 gene (ADS19165), the dermatopontin gene (C (ADS19163), the isocitrate dehydrogenase 2 gene (ADS19165), the major CC (ADS19171), the Sam68-like phosphotyrosine protein (ADS19170), the major CC (ADS19171), the Sam68-like phosphotyrosine protein (ADS19170), the major CC (ADS19177), and the tissue factor pathway inhibitor 2 gene (ADS19178). The invention also relates to marker gene-specific probes and CC pene (ADS19179) and real-time PCR primers specific for marker genes of the CC propertion (ADS19179) and antibodies specific for marker genes of the CC propertion (ADS1917) and antibodies specific for them; and kits comprising such probes microarrays, primers comprising probes microarrays or antibodies for identifying mesenchymal stem CC pathway inhibitor 2 gene and antibodies specific for marker genes of the CC propertion (ADS1917) and antibodies specific for them; and kits comprising probes microarrays, primers comprising probes microarrays, primers can define the primers and comprising the expression level of a comprising some sequence represents a specifically claimed human tissue factor pathway inhibitor 2 cDNA.

Sequence 1141 BP; 317 A; 246 C; 259 G; 319 T; 0 U; 0 Other;
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Query Match 99.8%; Score 977.4; DB 13; Length 1141; Best Local Similarity 99.9%; Pred. No. 3.7e-257; Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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14-MAR-2001;
10-AUG-2001;
19-SEP-2001;
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Meyers RB,
                                                                                                                                           Monahan JE, Gannavarapu M, Hoersch S, Kamatkar S,
Meyers RE, Morrisey MP, Olandt PJ, Sen A, Vieby
Bast RC, Lu K, Schmandt RE, Zhao X, Glatt K;
                                                                                                                                                8
                                                                                                                                                Kovatis SG;
O, Mills GB;
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Assessing whether a patient is afflicted with ovarian cancer, useful in assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and a non cancer patient.

Disclosure; Page 437; 481pp; English.

The present invention relates to a new method for assessing whether a gatient is afflicted with ovarian cancer. The method involves comparing the expression level of a marker in a patient sample and the normal level of expression of the marker in a control non-ovarian cancer sample, where the marker is selected from 363 cancer markers described in the general cancer tends of the invention is useful in diagnosing or characterising cancer, in detecting the presence of cancer as early as comparing cancer (e.g. patients having an enhanced risk of developing covarian cancer (e.g. patients having a familial history of ovarian cancer). The cancer markers may be used in the management and treatment concer). The cancer markers may be used in the management and treatment concer). The cancer markers may be used in the management and treatment concer). The cancer markers may be used in the management and treatment concer). The cancer markers may be used in the management and treatment concer). The cancer markers may be used in the management and treatment concer) creaters (e.g. bacterial or viral meningitis), concephalus or brain herniations), confident (e.g. cerebral oedems, hydrocephalus or brain herniations), confident (e.g. bacterial or viral meningitis or encephalitis), confident (e.g. bacterial or heart disorders (e.g. ischaemic heart (e.g. bacterial or historian cancer (e.g. ischaemic heart (e.g. bacterian cancer, motioning the progression of ovarian cancer, determining the progression of ovarian cancer, determining covarian cancer or at risk of developing ovarian cancer. The present nucleic acid invention

Sequence 1142 BP; 316 A; 248 C; 260 G; 318 T; 0 U; 0 Other;

ઇ 유·정 밁 8 밁 S 밁 S ঠ 밁 Matches Query Match Local 974; 199 139 301 241 181 121 79 61 19 μ. Similarity GGCTGTCGATTCTGCTGCTTTTTCCTGACGGAGGCTGCACTGGGCGCATGCTTCAGGAGC CAACAGGAAATAACGCGGAGATCTGTCTCCTGCCCCTAGACTACGGACCCTGCCGGGCCC TACTTCTCCGTTACTACGACAGGTACACGCAGAGCTGCCGCCAGTTCCTGTACGGGG CAACAGGAAATAACGCGGAGATCTGTCTCCTGCCCCTAGACTACGGACCCTGCCGGGCCC GGACGCCTTGCCCAGCGGGCCGGCCCGACCCCTGCACCATGGACCCCCGCTCGCCCCCTGG Conservative TCTCCGTTACTACGACAGGTACACGCCAGAGCTGCCGCCAGTTCCTGTACGGGG 99.3%; Score 972.2; DB 6; Pred. No. 9.9e-256; 0; Mismatches 3; Length 1142; Indels 0; 318 300 240 198 180 138 120 258 78

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361

GGTCCACAGAAAAGTATTTCTTTAATCTAAGTTCCATGACATGTGAAAAAATTCTTTTCCG

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RESULT 10
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  18-APR-2001;
10-MAY-2001;
09-NOV-2001;
13-NOV-2001;
29-NOV-2001;
                                                                                                                                                                                                                                                                                     Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema; antiinflammatory; antiasthmatic; non-small cell lung cancer; atclectasis; small cell lung cancer; benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity gneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
                                                                                                                              18-APR-2002;
                                                                                                                                                                                                             WO200286443-A2
                                                                                                                                                                                                                                                     Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABX76328 standard;
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; 2001US-0284770P.
; 2001US-0290492P.
; 2001US-0339245P.
; 2001US-0350666P.
; 2001US-0334370P.
                                                                                                                           2002WO-US012476.
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Best Local S
Matches 974
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99.7%;
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Pred. No. 9.9e-256;
0; Mismatches 3;
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Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.

G; 318 T, 0 Ġ 0 Other;

Indels Length 1142;

0

Gaps

0

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RESULT 11

ABX08764

ID ABX08

XX ABX08

XX ADGIC

XX ADGIC

XX Human

XX ADGIC

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19-APR-2001;
03-AUG-2001;
13-NOV-2001;
29-NOV-2001;
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  WPI; 2003-040681/03.
P-PSDB; ABU03481.
                                                          Murray R,
                                                                                                                                                                                                                                                                              14-PEB-2002;
                                                                                                                                                                                                                                                                                                                     10-OCT-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           angiogenesis-associated disease; cancer; cytostatic; gene therapy; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, angiogenesis-associated transcript; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Angiogenesis-associated human polynucleotide sequence
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                                                          Glymne R,
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; 2001US-00791390.
; 2001US-0285475P.
; 2001US-0310025P.
; 2001US-0350666P.
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                                                                                                 BIOTECHNOLOGY INC.
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Best Local S
Matches 974
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Detecting angiogenesis-associated transcript in a cell for diagnosing treating cancer by contacting a sample with a polynucleotide that exhibits changes in expression level as a function of time in tissue undergoing angiogenesis. and

Example 2; Page 205; 291pp; English

The present invention relates to methods and compositions for detecting CC an angiogenesis-associated transcript in a cell in a patient. The method CC involves contacting a biological sample from the patient with a CC polynucleotide that selectively hybridises to a sequence at least 80% CC identical to any of the angiogenesis-associated human polynucleotide sequences comprise genes angiogenesis-associated CC polynucleotide sequences comprise genes that exhibit changes in CC expression levels as a function of time in tissue undergoing CC angiogenesis. The method and the polynucleotide sequences of the CC invention are useful for diagnosing and treating angiogenesis and CC angiogenesis-associated diseases e.g. cancer. The polynucleotide sequences are also useful in the gene therapy of such disorders. The CC angiogenesis-associated protecins encoded by the polynucleotide sequences are useful as a vaccine for therapeutic and prophylactic immunisation. CC ABX08739.ABX08853 represent angiogenesis-associated polynucleotide

Sequence 1142 BP; 316 A; 248 C; 260 G; 318 T; 0 U; 0 Other;

660	ATACTGGCTGTGGAGGGAATGACAATAACTTTGTTAGCAGGGAGGATTGCAAACGTGCAT	Qy 601	Q
618	CTGCCAATGTGACTCGCTATTATTTTAATCCAAGATACAGAACCTGTGATGCTTTCACCT	Db 559	
600		Qy 541	Q
558		Db 499	
540	TCTGCGCACCAAAGAAAATTCCATCATTTTGCTACAGTCCAAAAAGATGAGGGGACTGTGCT	0у 481	0
498	GTGGGTGTCACCGGAACCGGATTGAGAACAGGTTTCCAGATGAAGCTACTTGTATGGGCT	Db 439	U
480		Qy 421	Q
438	GGTCCACAGAAAAGTATTTCTTTAATCTAAGTTCCATGACATGTGAAAAAATTCTTTTTCCG	Db 379	U
420		Qy 361	Q
378	GGATAGAAAAAGTTCCCAAAGTTTGCCGGCTGCAAGTGAGTG	Db 319	σ.
360		Qy 301	Q
318		Db 259	D.
300	GCTGCGAGGCAACGCCAACAATTTCTACACCTGGGAGGCTTGCGACGATGCTTGCT	Qy 241	Q
258	TACTTCTCCGTTACTACTACGACAGGTACACGCAGAGCTGCCGCCAGTTCCTGTACGGGG	Db 199	D.
240		Qy 181	Q
198	CAACAGGAAATAACGCGGAGATCTGTCTCCTGCCCCTAGACTACGGACCCTGCCGGGCCC	Db 139	Ħ
180		Qy 121	Q
138	GGCTGTCGATTCTGCTTTTTCCTGACGGAGGCTGCACTGGGCGATGCTGCAGGAGC	Db 79	Ö
120		Ογ 61	Q
78	9 GGACGCCTTGCCCAGCGGGCCGCCCGACCCCTGCACCATGGACCCCGCTCGCCCCTGG	Db 19	Ö
60		1	Q
0;	Matches 974; Conservative 0; Mismatches 3; Indels 0; Gaps	Matches 97	
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ID ADM38
XX ADM38
AC CAnce
XX Infla
KW Cetin
KW Cetin
KW detec
KW Wound
KW Vulne
XX Vound
KW 115-NC
XX 13-NC
PF 13-NC
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21-NOV-2001;
29-NOV-2001;
03-DEC-2001;
03-DEC-2001;
14-DEC-2001;
10-JAN-2002;
10-JAN-2002;
10-FEB-2002;
13-FEB-2002;
20-FEB-2002;
20-FEB-2002;
14-PR-2002;
15-JAR-2002;
16-JUN-2002;
16-JUN-2002;
22-JUL-2002;
22-JUL-2002;
23-JUL-2002;
24-JUL-2002;
25-JUL-2002;
29-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; differential expression; cancer; angiogenic disorder; fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularistaion syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.
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                                2002US-0347349P.
2002US-035250P.
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2002US-0359077P.
2002US-0368809P.
2002US-0377246P.
2002US-0377246P.
2002US-0396614P.
2002US-0397735P.
2002US-0397735P.
2002US-0397845P.
2002US-0397845P.
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R, Watson SR,
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Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
                                                                                                                                                                                    Glynne R,
B, Zlotnik
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A;
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CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclaristaion syndromes; scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a nucleic acid sequence of the invention.

Sequence 1142 BP; 316 A; 248 C; 260 G; 318 T; 0 U; 0 Other;

99.3%; Score 972.2; DB 11; Length 1142; 99.7%; Pred. No. 9.9e-256; tive 0; Mismatches 3; Indels 0; Gaps

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GGACGCCTTGCCCAGCGGGCCGCCCGACCCCTGCACCATGGACCCCGCTCGCCCCCTGG
                                          GGCTGTCGATTCTGCTGCTTTTTCCTGACGGAGGCTGCACTGGGCGATGCTGCTCAGGAGC
                                                                                                                         GGTCCACAGAAAAGTATTTCTTTAATCTAAGTTCCATGACATGTGAAAAAATTCTTTTTCCG
                                                                                                                                                                   CAACAGGAAATAACGCGGAGATCTGTCTCCTGCCCCTAGACTACGGACCCTGCCGGGCCC 180
TCTGCGCACCAAAGAAAATTCCATCATTTTGCTACAGTCCAAAAGATGAGGGGACTGTGCT 540
                                                                                                                                                                                             GGTCCACAGAAAAGTATTTCTTTAATCTAAGTTCCATGACATGTGAAAAAATTCTTTTCCG
                                                                                                                                                                                                                                TACTTCTCCGTTACTACGACAGGTACACGCAGAGCTGCCGCCAGTTCCTGTACGGGG
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Length 1142;

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798 780 738 720 678 600 558 540 498 480 438 420 378 360 318 300 120

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RESULT 13
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ID ADL83
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AC ADL83
AC ADL83
XX 17-JU
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KW Antia
KW Antia
KW Gene
KW Gene
KW Homo
XX 15-SE
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                                                                                                                                                                                                                                    Chiu H,
Wu TD,
                                                                             New PRO polypeptide, useful for diagnosing and treating a B cell related disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
                                       Claim 2, Fig 456; 695pp; English
                                                                                                                                                                      WPI; 2004-329389/30.
P-PSDB; ADL83255.
                                                                                                                                                                                                                                                                                                                                            16-SEP-2002; 2002US-0411392P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunosuppressive; Cytostatic; Antiathritic; Antirheumatic; Antianemic; Antiallargic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory; Gene Thorapy; PRO; B cell related disorder; cancer; fimmune-mediated inflammatory disease; human; gene; ss.
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                                                                                                                                                                                                                                                                                                  (GETH )
present invention relates to PRO
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proteins
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and their coding sequences
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Best Local Similarity
Matches 974; Conserv
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                                   GGAAAATTCGGAAGAAGCAATTTTAAACATTCTTAATATGTCATCTTGTTTTGTCTTTATG
                                                                                                                                                                                              ATACTGGCTGTGGAGGAATGACAATAACTTTGTTAGCAGGAGGATTGCAAACGTGCAT
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                                                                                    GTGCAAAAGCTTTGAAAAAAGAAAAAAGAAGATGCCAAAGCTTCGCTTTGCCAGTAGAATCC
                                                                                                                                                                                                                                                            CTGCCAATGTGACTCGCTATTATTTTAATCCAAGATACAGAACCTGTGATGCTTTCACCT
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Pred. No. 9.9e-256;
0; Mismatches 3;
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This invention relates to a novel isolated nucleic acid associated with CC bronchial cancer comprising 489 defined sequences given in the CC specification. The invention may be useful for the production of CC compounds with a cytostatic activity through the inhibition of expression CC cractivity of tumour-associated proteins. The novel DNA sequences and CC cancer or determining the risk of developing it and to screen for CC specific binding partners of the DNA or protein sequences, where the CC inding partners are potentially useful as agents for treating or CC diagnosing bronchial cancer. The DNA or protein sequences can also be used for prognosis, detection of metastases and for secondary treatment CC (of tumours that have been stabilised or are no longer detectable). CC Detecting abnormal expression of the DNA sequences parvides early CC diagnosis of bronchial cancers. The present sequence is that of a novel bronchial cancer-associated human gene sequence of the invention.
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  Sequence
                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 397; 1381pp; German.
                                                                                                                                                                                                                                                                             New nucleic acid, and derived proteins, useful for diagnosis of bronchial cancer and in screening for therapeutic and diagnostic agents.
                                                                                                                                                                                                                                                                                                                        WPI; 2004-786403/78.
P-PSDB; ADU06660.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bronchial cancer; cancer detection;
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                                                                                                                                                                                                                                                                                                                                                                               Mennerich D,
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HEIDEN CASTANOS-VELEZ
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ke S, Staub B, Hinzmann
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99.7%;
              995
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Pred. No. 9.9e-256;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a method for measurement of levels of visceral adipose tissue using markers. The invention also provides visceral adipose secreted proteins and their nucleic acids which are used as markers. The invention is useful in screening assays for identifying a compound that interacts with the visceral adipose secreted proteins and in the treatment of metabolic syndromera. The present sequence is human tissue factor pathway inhibitor 2 (TFPI-2; also termed as PPS, placental protein 5) coding DNA sequence which encodes one such adipose secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADZ87319 standard; DNA; 1142 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of nucleic acids having nucleotide bases with specific nucleic acid sequences, and polypeptides with specific amino acid sequences as markers in the diagnosis of visceral adipose tissue accumulation.
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DDBJ; D29992.
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/product= "Human tissue factor pathway inhibitor 2
protein"
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Search completed: March 11, 2006, 07:11:44 Job time : 637 secs

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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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100 04. Grove 070. DB 1. Tength 1104.	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /db_xref="taxon:9606" /clone="CSDDI060YJ11" /tissue_type="PLACENTA COT 25-NORMALIZED" /clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED" /clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED" /note="lst strand cDNA was primed with a NotI-oligo(dT) /note="lst strand cDNA was primed, double-strand cDNA was primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."	For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODIO60CE06QP1&c=4300.r. Location/Qualifiers 11104	CONTEXT: GENOSCOPE CONTEXT: GENOSCOPE GENOSCOPE - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster	Hominidae; Homo. 1 (bases 1 to 1104) Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001) On Feb 15, 2001 this sequence version replaced gi:31273791.	AL5519753 GI:45856764 AL551975.3 GI:45856764 EST. Homo sapiens (human) Homo sapiens (chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Primates; Catarrhini; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	AL551975 1104 bp mRNA linear EST 30-MAR-2004 AL551975 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA Clone CSODIO60YJ11 5-PRIME, mRNA sequence.

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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage:

BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

- Web: www.genoscope.cns.fr)

let strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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Contact : Feng Liang Email : fliang@lifetech.com URL :
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
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1 (bases 1 to 1002)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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ilarity 99.9%;
Conservative
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODIO36YK11"
/tissue_type="Placenta Cot 2:
/plasmid="pCMVSPORT_6"
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Pred. No. 1.6e-243;
0; Mismatches 1;
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                                                                                                                                                  Unpublished Contact : Feng Liang Email : fliang@lifetech.com URL Contact : Feng Liang Email : fliang@lifetech.com URL http://fulllength.invitrogen.com/ InVitroGen Corporal
                                                                                                                                                                                                                                                                                                                  CR605727 1006 bp mRNA linear full-length cDNA clone CS0DI042YP21 of Placenta Cot of Homo mapiens (human).

CR605727
       Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

By 191006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

BP 191006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
                                                                                                                                                                                             Hominidae; Homo.

1 (bases 1 to 1006)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Pull-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                  Homo sapiens (human)
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HTC; CNSLT_cDNA.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI042YP21"
/tissue_type="Placenta Cot
/plasmid="pCMVSPORT_6"
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Pred. No. 1.6e-243;
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`	₽ 3	B &	₿ �	99 80	Query Ma Best Loo Matches	ORIGIN	Bource	FEATURES	COMMENT	TITLE	REMARK	REFERENCE AUTHORS TITLE	SOURCE ORGANISM	ACCESSION VERSION KEYWORDS	RESULT 4 CR615838 LOCUS DEFINITION	B 1	§ §
241 GCTGCGAGGGCAACGCCAACAATTTCTACACCTGGGAGGCTTGCGACGATGCTTGCT	181 TACTTCTCCGTTACTACTACGACAGGTACACGCAGAGCTGCCGCCAGTTCCTGTACGGGG 240	121 CAACAGGAAATAACGCGGAGATCTGTCTCCTGCCCCTAGACTACGGACCCTGCCGGGCCC 180	61 GGCTGTCGATTCTGCTGACGGAGGCTGCACTGGGCGATGCTCAGGAGC 120	1 GGACGCTTGCCCAGCGGGCCGGACCCCCTGCACCATGGACCCCGGTCGCCCCCTGG 60	Query Match 99.8%; Score 977.4; DB 4; Length 1007; Best Local Similarity 99.9%; Pred. No. 1.6e-243; Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	/clone="CSODI075YF03" /tissue_type="Placenta Cot 25-normalized" /plasmid="pCMVSPORT_6"	ce 11007 /organism="Homo sapiens" /mol_type="mRNA" /db xref="taxon:9606"		 Web: www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned 	Genoscope. Direct Submission Submitted (20-0UL-2004) Genoscope - Centre National de Sequencage : BP 191 91,006 KWRY Cedex - FRANCE (8-mail : genraforenceros cos fe	CONTACT: Feng Liang Email: fliang@lifetech.com URL: CONTACT: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue 2 /base 1 to 1007	1 (bases 1 to 1007) 1 (bases 1 to 1007) 11,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization	Homo sapie Homo sapie Eukaryota; Mammalia;		CR615838 1007 bp mRNA linear HTC 21-JUL-2004 N full-length cDNA clone CSODI075YF03 of Placenta Cot 25-normalized	TGTTTGTGAGACTGAATTC	
REFERENCE AUTHORS TITLE JOURNAL	JOURNAL REMARK	REFERENCE AUTHORS	SOURCE ORGANISM	ACCESSION VERSION	RESULT 5 CR620705 LOCUS DEFINITION	Ο _Υ 9	φy dg	р Ş						D 5	\$ B \$	dg VQ	Ag Ag
2 (bases 1 to 1009) 2 (bases 1 to 1009) Genoscope. Direct Submission Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :	Unpublished Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faradav Avenue	Hominidae, Homo. 1 (bases 1 to 1009) Li,W.B., Gruber, C., Jessee, J. and Polayes, D.	HOMO SADIORS (DUNA. HOMO SADIORS (Numan) HOMO SADIORS HOMO SADIORS BUKARYOLA; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia: Rutheria: Ruarchortoglires: Primares: Catarrhini.		CR620705 1009 bp mRNA linear HTC 21-JUL-2004	961 TGTTTGTGAGACTGAATTC 979 963 TGTTTGTGAGACTGAATTC 981	901 TTTATATATAACTAGCTGCTATTCAAAIGTGAGICTACCATTTTTAATTTAIGGTTCAAC 960 	841 TIGGICATITATICACCAGITITIATIAATACAAGTCACTITITCAAAATITIGGATITI 900		GARARATICGARGARGARITITRARACATICTIRATRIGTCHTGTCTTTATRICGTCTTTATRICGTCTTTATRICGTCTTTATRICGTCTTTATRICGTCTTTATRICGTCTTTATRICGTCTTTATRICGTCATCTTGTCTTTGTCTTTATRICGTCATCTTGTCTTTGTCTTTATRICGTCATCTTGTCTTTATRICGTCATCTTGTCTTTATRICGTCATCTTGTCTTTATRICGTCATCTTGTCTTTATRICGTCATCTTGTCTTTATRICGTCATCTTGTCTTTATRICGTCATCTTGTCTTTATRICGTCATCTTGTCTTTATRICGTCATCTTGTCTTTATRICGTCATCTTGTCTTTATRICGTCATCTTGTCTTGTCTTTATRICGTCATCTTGTCTTTATRICGTCATCTTGTCTTTATRICGTCATCTTTATRICGTCATCTTTATRICGTCATCTTGTCTTTATRICGTCATCTTATRICGTCATCTTTATRICGTCATCTTATRICGTCATCTTATRICGTCATCTTTATRICGTCATCTTATRICGTCATCTTATRICGTCATCTTATRICGTCATCTTATRICGTCATCTTATRICGTCATCTTATRICGTCATCATCATCATCATCATCATCATCATCATCATCATCAT	51 GTGCAAAAGCTTTGAAAAAGAAAAAGAAGATGCCAAAAGCTTGGCTTTGCCAGTAGAATCC 63 GTGCAAAAGCTTTGAAAAAGAAAAAGAAGATGCCAAAAGCTTCGCTTTGCCAGTAGAATCC 63 GTGCAAAAGCTTTGAAAAAAAAAAAAAAAAATGCCAAAAGCTTCGCTTTTGCCAGTAGAATCC	OL ATACTEGCTET/GGAAGGAATTACATTATCTTTAGCAGGAGGATTGCAAACGTGCAT	41 CTGCCAATGTGACTCGCTATTATTTTAATCCAAGATACAGAACCTGTGATGCTTTCACCT	*81 TCTGCGCHCCHANGSHAMTTCCATCATTTTGCTACAGTCCAAAAGATGAGGGACTGTGCT 540	GTGGGTGTCACCGGAACCGGATTGAGAACAGGTTTCCAGATGAAGCTACTTGTATGGGCT	361 GGTCCACAGAAAAGTATTTCTTTAATCTAAGTTCCATGACATGTGAAAAAATTCTTTTCCG 420 	301 GGATAGAAAAAGTTCCCAAAGTTTGCCGGCTGCAAGTGAGTG

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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="C90D1064YL18"
/tissue_type="placenta Cot 2
/plasmid="pCMVSPORT_6"
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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Direct Submission
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Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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1 (bases 1 to 1028)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 1031)
Li, W.B., Gruber, C.,
                                                                                       CR615468 1031 bp n full-length cDNA clone CS0DI068YJ03 of Home Bapiens (human) CR615468 CR615468 1 GI:50496275 HTC; CNSLT_CDNA.
                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
                                                              Homo sapiens (human)
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Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecok V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODIO68YJ03"
/tissue_type="Placenta Cot
/plasmid="pCWVSPORT_6"
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Query Match Best Local : Matches 97: Qy 1	PATURES BOUTCE	COMMENT	JOURNAL REMARK REFERENCE REFERENCE AUTHORS TITLE JOURNAL	ORGANISM REFERENCE AUTHORS TITLE	CR612082 LOCUS DEFINITION ACCESSION VERSION KEYWORDS		<u> </u>	B & B &	
Query Match 99.8%; Score 977.4; DB 4; Length 1033; Best Local Similarity 99.9%; Pred. No. 1.6e-243; Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0; 1 GGACGCCTTGCCCAGCGGGCCGGCCCGTCGACCCCCTGGACCCCCCTGGACCCCCCTGGACCCCCCTGGACCCCCCTGGACCCCCTGGACCCCCTGGACCCCCTGGACCCCCTGGACCCCCTGGACCCCCCTGGACCCCCTGGACCCCCTGGACCCCCTGGACCCCCCTGGACCCCCCTGGACCCCCCTGGACCCCCCTGGACCCCCCTGGACCCCCCTGGACCCCCCTGGACCCCCCTGGACCCCCCTGGACCCCCCCTGGACCCCCCTGGACACACAC	IN 1033 10 1. 1033 /organism="Homo sapiens" /mol_type="mRNA" sapiens" /db_xref="taxon:9606" /clone="CSODI012YJ24" /tissue_type="Placenta Cot 25-normalized" /plasmid="pcMVSPORT_6"	BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr) - Web: www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.	g@llfetech.com URL : InVitroGen Corporation 1600	Homo Bukar Mamma Homin 1 (b Li, W.		TGTTTGTGAGACTGAATTC 979	841 TGGTGATTTATCACCAGTTTTATTATACAAGTCACTTTTCAAAAATTTGGATTT 900		GTGCAAAAGCTTTGAAAAAGAAAAAGAAGATGCCAAAGCTTCGCTTTGCCAGTAGAATCC
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Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVVR cedex - FRANCE (B-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a
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1 (bases 1 to 1034)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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HTC; CNSLT_cDNA.
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
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/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 1.6e-243;
0; Mismatches 1;
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                                                                                                                        Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage:
BP 191006 EVRY cedex - FRANCE (B-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                                                                                                                                                      Genoscope.
                                                                                                                                                                                                                                                                                                                                     Contact : Feng Liang Email : fliang@lifetech.com URL
http://fulllength.invitrogen.com/ InVitroGen Corporat
                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                        Hominidae; Homo.

1 (bases I of 1038)

Li W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CR618958.1 GI:50499765
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/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="reaxon:9606"
/clone="CSODIO58YM18"
/tissue_type="Placenta Cot 2
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TGTTTGTGAGACTGAATTC 979
                                                     TTTATATATAACTAGCTGCTATTCAAATGTGAGTCTACCATTTTTAATTTATGGTTCAAC
                                                                         TTTATATATAACTAGCTGCTATTCAAATGTGAGTCTACCATTTTTAATTTATGGTTCAAC
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Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 19 19106 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact : Feng Liang Email : fliang@lifetech.http://fulllength.invitrogen.com/ InVitroGen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 1039)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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HTC; CNSLT_cDNA.
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CR624861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CR624861 1039 bp mRNA linear full-length cDNA clone CS0DI016YN22 of Placenta Cot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Faraday Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                         GANCGCCTTGCCCAGCGGGCCCCGCCCCGACCCCCTGCACCACCATGGACCCCCGCTCGCCCCCTGG
     GGTCCACAGAAAAGTATTTCTTTAATCTAAGTTCCATGACATGTGAAAAAATTCTTTTCCG
                                                                 GCTGCGAGGGCAACGACAATTTCTACACCTGGGAGGCTTGCGACGATGCTTGCGA
                                                                                                                                                                                            TACTTCTCCGTTACTACGACAGGTACACGCAGAGCTGCCGCCAGTTCCTGTACGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODIO16YN22"
/tissue_type="Placenta Cot 2"
/plasmid="pCMVSPORT_6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 977.4; DB 4;
Pred. No. 1.6e-243;
0; Mismatches 1;
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Corporation 1600
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25-normalized
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CR621074
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AUTHORS
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Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

HP 191 www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
                                                                                                                                                                                   Hominidae; Homo.

1 (bases 1 to 1042)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished
                                                                                                                                                                                                                                                                                                                                                     CR621074 1042 bp mRNA linear full-length cDNA clone CS0DI012YA05 of Placenta Cot of Homo mapiens (human).

CR621074
                                                                                                                         Faraday Avenue
2 (bases 1 to 1042)
                                                                                                                                                     Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation
                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                         CR621074.1 GI:50501881
HTC; CNSLT_CDNA.
                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
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                                GTGCAAAAGCTTTGAAAAAGAAAAAAAGATGCCAAAGCTTCGCCTTTGCCAGTAGAATCC
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      TTGGTGATTTATTCACCAGTTTTTATTAATACAAGTCACTTTTTCAAAAATTTGGATTTT
                                                                                                                                                        GTGCAAAAGCTTTGAAAAAGAAAAAGAAGATGCCAAAGCTTCGCTTTGCCAGTAGAATCC
                                                                                                                                                                                                                  ATACTGGCTGTGGAGGGAATGACAATAACTTTGTTAGCAGGGAGGATTGCAAACGTGCAT
                                                                                                                                                                                                                                                                            CTGCCAATGTGACTCGCTATTATTTTAATCCAAGATACAGAACCTGTGATGCTTTCACCT
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSDDI012YA05"
/tissue_type="Placenta_Cot_2"
/plasmid="pCMVSPORT_6"
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Pred. No. 1.6e-243;
0; Mismatches 1;
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Query Match Best Local; Matches 97 Qy 1 Db 32 Qy 61 Db 92 Qy 121 Db 152 Qy 181 Db 212	ORIGIN	COMMENT	REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE JOURNAL REMARK	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 13 CR611856 LOCUS DEFINITION	B 3	B 8	дb
Whatch 99.8%; Score 977.4; DB 4; Length 1046; Local Similarity 99.9%; Pred. No. 1.6e-243; neb 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0; 1 GGACGCCTTGCCCAGCGGGCCCCCCCCCCCCTGCACCCCTGCACCCCCCCC	/pi /db /c1 /c1	1st end intc was divi	2 (Dates 1 to 1046) 2 (Dates 1 to 1046) Genoscope. Direct Submission Submitted (20-JUL-2004) Genoscope - Centre National de Sequence BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.ci - Web : www.genoscope.cns.fr)		3		961 TGTTTGTGAGACTGAATTC 979	901 TTTATATATAACTAGCTGCTATTCAAATGTGAGTCTACCATTTTTAATTTATGGTTCAAC 960	
RESULT 14 CR 60533 LOCUS LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL REMARK	9 Q B 4	5 B 5 B	2	B & B & 1	B & B &	Db Q	B &	Qy Db	Qy 2
CR605333 CR605333 CR605333 CR605333 CR605333. GI:50486140 CR605333. GI:50486140 HTC; CNSLT_CDNA. HOMO sapiens (human) HOMO sapiens (human) HOMO sapiens (human) HOMO sapiens (burnan) HOMO sapiens (human) HOMO sapiens (hu	32 TITATATATAACTAGCTGCTATCAAARGTGAGTCTACCATTTTTAATTTATGGTTCAAC 61 TGTTTGTGAGACTGAATTC 979	312 GCTTATTTGCCTTTATGTTGTATCIGAAGAATAATAIGACAGCAIGAGGAAACAAAICA 871 341 TIGGTGATTTATTCACCAGTTTTTATTAATACAAGTCACTTTTTCAAAAATTTTGGATTTT 900 371 TIGGTGATTTATTCACCAGTTTTTATTAATACAAGTCACTTTTTAAAAAATTTTGGATTTT 931 372 TIGGTGATTTATTCACCAGTTTTTATTAATACAAGTCACTTTTTAAAAAATTTTGGATTTT 931	GGAAAATTCGGAAGAAGCAATTTTAAACATTCTTAATATGTCATCTTGTCTTTGTCTTTATG	ATACTGGCTGTGGAGGAATGACAATAACTTTGTTAGCAGGAGGATTGCAAACGTGCAT	181 TCTGCGCACCAAACAAAATTCCATCATTTTGCTACAGCTCCAAAAGATGAGGGACTGTGCT 540	121 GTGGGTGTCACCGGAACCGGATTGAGAACAGGTTTCCAGATGAAGCTACTTGTATGGGCT 480)61 GGTCCACAGAAAAGTATTTCTTTAATCTAAGTTCCATGACATGTGAAAAAATTCTTTTCCG 420)01 GGATAGAAAAAGITCCCAAAGTTTGCCGGCTGCAAGTGAGTGTGGACGACCAGTGTGAGG 360 	241 GCTGCGAGGGCAACGCCAACAATTTCTACACCTGGGAGGCTTGCGACGATGCTTGCT

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Matches 978; Conserv
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Genoscope.
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1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                division of Invitrogen.
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              GTGCAAAAGCTTTGAAAAAAGAAAAAAGATGCCAAAGCTTCGCTTTGCCAGTAGAATCC
                                                           ATACTGGCTGTGGAGGGAATGACAATAACTTTGTTAGCAGGGAGGATTGCAAACGTGCAT
                                                                                                              CTGCCAATGTGACTCGCTATTATTTTAATCCAAGATACAGAACCTGTGATGCTTTCACCT
                                                                                                                                        TCTGCGCACCAAAGAAATTCCATCATTTTGCTACAGTCCAAAAGATGAGGGACTGTGCT
                                                                                                                                                        TCTGCGCACCAAAGAAAATTCCATCATTTTGCTACAGTCCAAAAGATGAGGGACTGTGCT
                                                                                                                                                                                                                                      GGTCCACAGAAAAGTATTTCTTTAATCTAAGTTCCATGACATGTGAAAAAATTCTTTTCCG
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/db xref="taxon:9606"
/clone="CS0DIO75YB17"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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Pred. No. 1.6e-243;
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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Submitted (20-JUL-2004) Genoscope - Centre National de
BP 191 91006 EVRY cedex - FRANCE (B-mail : segref@genos
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1 (Dases 1 to 1050)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
Unpublished

Contact: Feng Liang Email: fliang@lifetech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CR607266 1050 bp mRNA linear HTC 21-JUL-2004 full-length cDNA clone CS0DI066YA08 of Placenta Cot 25-normalized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://fulllength.invitrogen.com/
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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CR607266
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                       GGCTGTCGATTCTGCTGCTTTTTCCTGACGGAGGCTGCACTGGGGCGATGCTGCTCAGGAGC 120
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                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODIO65YAO8"
/tissue_type="Placenta_Cot_2
/plasmid="pCMVSPORT_6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : Peng Liang Email : fliang@lifetech.com URL
fulllength.invitrogen.com/ InVitroGen Corporat
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Pred. No. 1.6e-243;
0; Mismatches 1;
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Search completed: March 11, 2006, 08:20:02 Job time: 4768 secs

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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
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1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

7: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*

9: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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             US-08-147-710-1
US-08-458-090-1
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US-09-949-016-1187
US-09-949-016-864
US-09-949-016-864
US-09-736-457-64
US-09-736-457-64
US-09-614-1248-64
US-09-589-184-64
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Sequence 864, Appli
Sequence 64, Appli
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; Sequence 1, Ap
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FEATURE:
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59	59	59	59	59	59	59	59	59	59	59	59	59	59.6	62.6	64.2	67	153	153	153	153
6.0	6.0	6.0	6.0	6.0		6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.1	6.4	6.6	6.8	15.6	15.6	15.6	15.6
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US-09-627-676-1	US-09-054-782-1	US-10-000-489-51	US-10-000-489-95	US-10-000-489-47	US-09-949-016-1529	PCT-US95-09377-1	US-08-854-764-1	US-08-321-658B-7	US-08-446-646-8	US-08-026-145-1	US-09-763-565-3	US-09-763-565-1	US-09-388-183-4	US-09-910-430-7	US-08-554-161-1	US-09-388-183-1	US-09-904-621-14	US-08-457-887-14	US-08-458-090-14	US-08-147-710-14
Sequence 1, Appli	Sequence 1, Appli	Sequence 51, Appl	Sequence 95, Appl	Sequence 47, Appl	Seguence 1529, Ap	Sequence 1, Appli	Sequence 1, Appli	Sequence 7, Appli	Sequence 8, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 1, Appli	Sequence 4, Appli	Sequence 7, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 14, Appl	Sequence 14, Appl	Sequence 14, Appl	•

ALIGNMENTS

GENERAL INFORMATION: MOLECULE TYPE: CORIGINAL SOURCE: ORGANISM: Homo APPLICANT: Sprecher, Cindy A. APPLICANT: Kisiel, Walter APPLICANT: Foster, Donald C. TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS TITLE OF INVENTION: METHODS RELATING THERETO NUMBER OF SEQUENCES: 15 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy IMMEDIATE SOURCE: CLONE: J-2-11 CORRESPONDENCE ADDRESS: TOPOLOGY: linear COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS COUNTRY: U CITY: Seattle TYPE: nucleic acid Application US/081/7710 B: ZymoGenetics, Inc. 4225 Roosevelt Way, N.E. USA Homo sapiens E: Placenta CDNA Floppy disk

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; NAME/KEY:
; LOCATION:
US-08-147-710-1
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Best Local Similarity 100.0%;
Matches 979; Conservative C
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                                                TTTATATATAACTAGCTGCTATTCAAATGTGAGTCTACCATTTTTAATTTATGGTTCAAC 960
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    TGTTTGTGAGACTGAATTC
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Pred. No. 1.8e-264;
0; Mismatches 0; Indels
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Patent No.
                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 979; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 979 base pairs
TYPE: nucleic acid
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CITY: Seattle
STATE: WA
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ZIP: 98102
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/458,090
PILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 93-14D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
INFORMATION FOR SEQ ID NO: 1:
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APPLICANT: Speecher, Cindy A.

APPLICANT: Kisiel, Walter

APPLICANT: Kisiel, Walter

TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS AND

TITLE OF INVENTION: METHODS RELATING THERETO

NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Placenta
IMMEDIATE SOURCE:
CLONE: J-2-11
FEATURE:
NAME/KEY: CDS
LOCATION: 39..746
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ADDRESSEE: ZymoGenetice, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1, Application US/08458090
5. 5728674
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                               CAACAGGAAATAACGCGGAGATCTGTTCTCCTGCCCCTAGACTACGGACCCTGCCGGGCCC
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CAACAGGAAATAACGCGGAGATCTGTCTTCCTGCCCCTAGACTACGGACCCTGCCGGGCCC
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RESULT 3
US-08-457-887-1
                                                         Sequence 1, Application US/08457887

Sequence 1, Application US/08457887

Patent No. 5914315

GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Kisiel, Walter
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS AND TITLE OF INVENTION: METHODS RELATING THERETO
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Bastlake Avenue East
           CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
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; NAME/KEY:
; LOCATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,887
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 93-14D1
REFERENCE/DOCKET NUMBER: 93-14D1
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Best Local
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TELEPHONE: 206-442-6673
TELEPAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 1:
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LENGTH: 979 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUB TYPE: Placenta
IMMEDIATE SOURCE:
CLONE: J-2-11
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PRIOR APPLICATION DATA:
APPLICATION INMBER:
APPLICATION INMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
AREGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELEFONMUNICATION INFORMATION:
TELEFPHONE: (650) 855-0555
TELEFAX: (650) 855-0555
TELEFAX: (650) 805-4166
INFORMATION FOR SEQ ID NO: 1378:
SEQUENCE CHARACTERISTICS:
LENGTH: 979 base pairs
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US-09-016-434-1378
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Patent No. 6500938

GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS: INC.
                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WOR'D PERFECT 6.1 for Windows/MS-DOS 6.:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION.
                                                                                                                                                                                                                                                                                                                                                                 STATE: CALIFORNIA
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; STRANDEDNESS: sing
; TOPOLOGY: linear
; TOMEDIATE SOURCE:
; LIERARY: GENBANK
; CLONE: 9341149
US-09-016-434-1378
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  TTTATATATAACTAGCTGCTATTCAAATGTGAGTCTACCATTTTTAATTTATGGTTCAAC
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Sequence 1, Application US/09904621

Patent No. 6656746

GENERAL INFORMATION:

APPLICANT: Sprecher, Cindy A.

APPLICANT: Syecher, Conald C.

TITLE OF INVENTION: MOTHODS RELATING THERETO

FILE REFERENCE: 93-14D3

CURRENT APPLICATION NUMBER: US/09/904,621

CURRENT APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/265,627

PRIOR RILING DATE: EARLIER APPLICATION NUMBER: 09/265,627

PRIOR RELICATION NUMBER: EARLIER APPLICATION NUMBER: 09/265,627

PRIOR RELICATION NUMBER: EARLIER APPLICATION NUMBER: 09/265,627

PRIOR RELICATION NUMBER: EARLIER APPLICATION NUMBER: 5,455,338

PRIOR RELICATION NUMBER: EARLIER PILING DATE: 1999-03-09

PRIOR RELICATION NUMBER: EARLIER FILING DATE: 1993-11-05

NUMBER OF SEQ ID NOS: 15

SOPTWARE: PASTSEQ for Windows Version 3.0

SEQ ID NO 1

SEQ ID NO 1

SEQ ID NO 1

SEQ ID NO 6

CORGANISM: Homo Sepiens

PEATURE:

NAME/KEY: CDS

LOCATION: (39)...(746)
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                                    GTGGGTGTCACCGGAACCGGATTGAGAACAGGTTTCCAGATGAAGCTACTTGTATGGGCT 480
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APPLICANT VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CCURRENT APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1187
LENGTH: 1583
TYPE: DNA
ORGANISM: Human
US-09-949-016-1187
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US-09-949-016-1187
Sequence 1187, Application US/09949016
; Patent No. 6812339
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APPLICANT: VENTER, J.
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                                                                                                                                                             Watch 99.8%; Local Similarity 99.9%;
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                                                                                                                                            Conservative
                                                                                                                                          Score 977.4; DB 3;
Pred. No. 6.4e-264;
0: Mismatches 1;
                                                                                                                                                                              Length 1583;
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Sequence 864, Application US/09949016
PATENT NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANTION: WITH HUMAN DISEASE, METHODS OF DETECTION OF INTERPRENEES CLO01307
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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Matches 974; Conserv
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                                                        GTGCAAAAGCTTTGAAAAAGAAAAAAAGATGCCAAAAGCTTCGCCTTTGCCAGTAGAATCC
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          GCTTATTTGCCTTTATGGTTGTATCTGAAGAATAATATGACAGCATGAGGAAACAAATCA
                                               GGAAAATTCGGAAGAAGCAATTTTAAAACATTCTTAATATGTCATCTTGTTTTGTCTTTATG
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99.7%;
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Pred. No. 1.6e-262;
0; Mismatches 3;
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Bequerice 2, Application Ug/08817145
Patent No. 6025329
GENERAL INFORMATION:
APPLICANT: UTSUMI, Jun
APPLICANT: SUDO, TeyBuo
APPLICANT: TANAKA, YaBuhiko
APPLICANT: TANAKA YABUhiko
APPLICANT: TANAKA YABUHIKO
APPLICANT: TANAKA TABUHIKO
APPLICANT: TANAKA TABUHIKO
APPLICANT: TANAKA TABUHIKO
APPLICANT. OF INVENTION: THERAPEUTIC
TITLE OF INVENTION: DISEASES
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LOCATION:
US-08-817-145-2
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CORRESPONDENCE ADDRESS:
ADDRESSE: Birch, Stewart, Kölasch & Birch, LL.
STREET: P.O. Box 747
CITY: Falls Church
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/817,345
FILING DATE: 02-JUL-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 760-230P
                                                                                                                        Query Match
Best Local Similarity
Matches 978; Conserv
                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEPAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1140 base pairs
                                                                                                                                                                                                                 MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                                            LENGTH: 1140 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
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                                                                                  TGTTTGTGAGACTGAAT 977
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                                                                      GGACGCCTTGCCCAGC-GGCCGCCCGACCCCCTGCACCATGGACCCCGCTCGCCCCCTGG
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llarity 99.9%;
Conservative
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Pred. No. 4.5e-261;
0; Mismatches 0;
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; Sequence 64, Application US/09702705; Patent No. 6504010; GENERAL INFORMATION: APPLICANT: Wang, Tongtong APPLICANT: Lodes, Michael A.; APPLICANT: Lodes, Michael A.; APPLICANT: Panger, Gary APPLICANT: Vedvick, Tom APPLICANT: Carter, Darrick; APPLICANT: Retter, Marc
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US-09-702-705-64
; Sequence 64, A)
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APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
ITITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
ITITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 64
LENGTH: 528
TYPE: DNA
ORGANISM: Homo sapien
FEATURE;
NAME/KEY: misc_feature
LOCATION: (1)...(528)
OTHER INFORMATION: n = A,T,C or G
US-09-702-705-64
  Sequence 64, Application US/09736457
Patent No. 6509448
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Panger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Marc
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
                                                                                                                        RESULT 10
US-09-736-457-64
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; Pred. No. 2.7e-115;
42; Mismatches 20;
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TYPE: DNA

TORANISM: Homo sapien

FRATURB:

NAME/KEY: misc feature

LOCATION: (1)...(528)

OTHER INFORMATION: n = A

US-09-736-457-64
                                                                                                                     US-09-614-124B-64
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APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILLE REFERENCE: 210121.478015
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FASTSEQ for Windows Version 3.0
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APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Ton
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
                                                                                      GENERAL INFORMATION:
                                                                                                Sequence 64, Application Patent No. 6630574
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SEQ ID NO 64
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                GTGGGTGTCACCGGAACCGGATTGAGAACAGGTTTCCAGATGAAGCTACTTGTATGGGCT
                                                          GGTCCACAGAAAAGTATTTCTTTAATCTAAGTTCCATGACATGTGAAAAAATTCTTTTCCG
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GTGGGNGTCACCGG-ACCGGATTGAGAACANGTTTGCAGATGANGCTACTGGGATGGGCT
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: PASTSEQ for Windows Version 3.0
; SEQ ID NO 64
; LENGTH: 528
; TYPE: DNA
; ORGANISM: Homo sapien
; PEATURE: misc feature
; LOCATION: (1)...(528)
; OTHER INFORMATION: n = A,T,C or G
US-09-614-124B-64
               Sequence 64, Application US/09671325
Patent No. 6667154
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND
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US-09-671-325-64
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ORMATION:

Wang, Tongtong
Bangur, Chaitanya S
Lodes, Michael A.
Franger, Gary
T: Vedvick, Tom
T: Carter, Darrick
TT: Retter, Marc
MT: Mannion, Jane
NT: Fan, Liqun
NT: Fan, Liqun
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                      AND METHODS
                      FOR THE THERAPY AND
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; LENGTH: 528
; TYPE: DNA
; ORGANISM: Homo mapien
; PEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(528)
; OTHER INFORMATION: n = A,T,C ox
US-09-671-325-64
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Lodes, Michael A.
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AN
TITLE OF INVENTION: DIAGNOSIS OF LU
FILE REFERENCE: 210121.478C8
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US-09-589-184-64
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                                                                                                                                               Sequence 64, Application US/09589184 Patent No. 6686447
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/671,325
CURRENT FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 1825
SOFTWARE: PastSEQ for Windows Version 3.0
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87.5%; Pred. No. 2.7e-115;
tive 42; Mismatches 20;
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                AND METHODS FOR THERAPY AND LUNG CANCER
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CURRENT APPLICATION NUMBER: US/09/589,184
CURRENT FILING DATE: 2000-06-05
NUMBER OF SEQ ID NOS: 827
SOFTWARE: FASKSEQ for Windows Version 3.0
SEQ ID NO 64
LENGTH: 528
TYPE: DNA
ORGANISM: Homo sapien
PRATURE:
NAME/KEY: misc_feature
CONTION: (1)...(528)
OTHER INFORMATION: n = A,T,C or G
US-09-589-184-64
Sequence 64, Application US/09658824

Patent No. 6746946

GENERAL INFORMATION:

APPLICANT: Wang, Tongtong

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Lodes, Michael A.

APPLICANT: Lodes, Michael A.

APPLICANT: Vedvick, Tom

APPLICANT: Vedvick, Tom

APPLICANT: Retter, Marc

APPLICANT: Retter, Marc

APPLICANT: Rannion, Jane

APPLICANT: Fan, Liqun

ITITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE REFERENCE: 210121.478C11

CURRENT APPLICATION NUMBER: US/09/658,824
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Pred. No. 2.7e-115;
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Sequence 64, Application US/10017754

Patent No. 6658204

GENERAL INFORMATION:
APPLICANT: Henderson, Robert A.
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Retter, Marce W.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: McNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; CURRENT FILING DATE: 2000-09-08; NUMBER OF SEQ ID NOS: 1788; SOFTWARE: FastSEQ for Windows Ver. SEQ ID NO 64; SEQ ID NO 64; SEQ ID NO 64; SEQ ID NO 64; ORGANISM: Homo sapien FABATURE: NAME/KEY: misc_feature; LOCATION: (1)...(528) OTHER INFORMATION: n = A,T,C or G
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US-10-017-754-64
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87.5%; Pred. No. 2.7e-115;
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CURRENT APPLICATION NUMBER: US/10/017,754
CURRENT FILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 2004
SOFTMARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 64
LENGTH: 528
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
NAME/KEY: misc_feature
COCATION: 374,443,444,452,476,489,515,52:
OTHER INFORMATION: n = A,T,C or G
US-10-017-754-64
Search completed: March 11, 2006, 06:08:17 Job time : 226 secs
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                     Published_Applications_NA_Main:*

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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
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US-10-901-321-23
US-09-814-353-19662
US-10-904-817-143
US-10-904-817-143
US-10-904-817-1625
US-10-1428-487-6
US-10-1428-487-6
US-10-956-157-6860
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Sequence 1, Appli
Sequence 1379, Ap
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Sequence 1, Appli
Sequence 145, App
Sequence 23, Appl
Sequence 609, App
Sequence 143, App
Sequence 315, Appl
Sequence 315, Appl
Sequence 6, Appli
Sequence 6, Appli
Sequence 1625, Appl
Sequence 1625, Appl
Sequence 1625, Appl
Sequence 25, Appl
Sequence 210, Appl
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	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
	14, Appl	14, Appl	29, Appl	98, Appl	469, App	2271, Ap		12714, A	20649, A	20622, A	133716,	470, App	22448, A	10074, A	13780, A	23202, A	•	•	•	•	64, Appl	•

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rccer1	JAAATA JAAATA	CATTO	TIGCC	100 larity 100 Conservative	1-1 1-1 1-2 1 Application US/ US2002098560A1 FORMATION: Sprecher, Cindy Kisiel, Walter POSTEY, Donald INVENTION: MOVEL INVENTION: METHO INVENTION: METHO INVENTION: MUMBER: ILIATION NUMBER: ILIATION NUMBER: ING DATE: EARLIER ICATION NUMBER: ING DATE: EARLIER ING DATE: TO NUMBER: ING DATE: TO NU
ACTAC	ACGCG	Tecre	CAGCGC	100.0%; 100.0%;	4-621-1 Ce 1, Application US/09904621 No. US20020098560A1 L INFORMATION: CANT: Sprecher, Cindy A. CANT: FOSTER, WOYEL HUMAN KUNIT: OP INVENTION: AND OP INVENTION: METHODS RELATING REFERENCE: 93-14D3 OF INVENTION INVEST: US/09/904, NT FILING DATE: 2001-07-13 APPLICATION NUMBER: EARLIER APPL FILING DATE: EARLIER FILING DATE APPLICATION NUMBER: EARLIER APPL FILING DATE: EARLIER FILING DATE APPLICATION NUMBER: FILING DATE APPLICATION STANLIER FILING DATE APPLICATION NUMBER: FILING DATE APPLICATION NOBELIER FILING DATE APPLICATION
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RESULT 2
US-10-305-720-1378
US-10-305-720-1378
Sequence 1378, Application US/10305720
Publication No. US20040010136A1
GENERAL INFORMATION:
APPLICANT: AL-YOUNG, Janice K.; Seilhamer, Jeffrey J.
TITLE OF INVENTION: Composition for the Detection of Signaling Path
FILE REFERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: 09/016,434
PRIOR FILING DATE: 1998-01-30
UNMBER OF SEQ ID NOS: 1490
SOPTWARE: PERL PROGram
SEQ ID NO 1378
FILENGTH: 979
LENGTH: 979
TYPE: DNA
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Pred. No. 2.8e-247;
; Mismatches 0;
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Sequence 1, Application US/10680684

Publication No. US20040253686A1

GENERAL INFORMATION:

APPLICANT: Sprechar, Cindy A.

APPLICANT: Kisiel, Walter

APPLICANT: FOSTER, DOWAL HUMAN KUNITZ-TYPE INHIBITORS

TITLE OF INVENTION: AND

TITLE OF INVENTION: WETHODS RELATING THERETO

FILE REFERENCE: 93-14D3

CURRENT FILING DATE: 2003-10-07

PRIOR APPLICATION NUMBER: US/10/680,684

CURRENT FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US/99/904,621

PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/99/903-09

PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: 09/265,627

PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: 09/265,627

PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: 5,455,338

PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: 5,455,338

PRIOR FILING DATE: PRIOR FILING DATE: 1993-11-05

NUMBER OF SEQ ID NOS: 15

SOPTWARE: FastSEQ for Windows Version 3.0

LENGTH: 979
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; TYPE: DNA
; ORGANISM: Homo sapiens
; EEATURE:
; NAME/KEY: CDS
; LOCATION: (39)...(746)
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                                      ; SEQ ID NO 1
; LENGTH: 979
; TYPE: DNA
; TYPE: DNA
; CRGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (39)...(746)
US-10-800-057-1
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APPLICANT: Kisiel, Walter
APPLICANT: Kisiel, Walter
APPLICANT: Kisiel, Walter
APPLICANT: FOSTER: Donald C.
TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS
TITLE OF INVENTION: MATHODS RELATING THERETO
FILE REFERENCE: 93-14D3
CURRENT APPLICATION NUMBER: US/10/800,057
CURRENT FILING DATE: 2004-03-12
PRIOR APPLICATION NUMBER: US/10/680,684
PRIOR FILING DATE: 2003-10-07
PRIOR APPLICATION NUMBER: US/09/904,621
PRIOR APPLICATION NUMBER: US/09/904,621
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: 5,455,338
PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: 5,455,338
PRIOR FILING DATE: PRIOR FILING DATE: 1993-11-05
NUMBER OF SEQ ID NOS: 15
SECTION NO.
Query Match 100.0%; Score 979; DB 8; Length 979; Best Local Similarity 100.0%; Pred. No. 2.8e-247; Matches 979; Conservative 0; Mismatches 0; Indels
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APPLICANT: BENSON, Darin R.
APPLICANT: Kalos, Michael D.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Jiang, Yuqiu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.566
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 145
SEQ ID NO 145
LENGTH: 1172
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 979; Conser
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              GTGCAAAAGCTTTGAAAAAAGAAAAAGAAGATGCCAAAGCTTCGCCTTTGCCAGTAGAATCC
                                                               ATACTGGCTGTGGAGGGAATGACAATAACTTTGTTAGCAGGGAGGATTGCAAACGTGCAT
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Sequence 23, Application US/10991321

Publication No. US20050112675A1

GENERAL INFORMATION:
APPLICANT: Kochen, Jarema Peter
APPLICANT: Rosinski, James Andrew
TITLE OF INVENTION: Specific Markers for Metabolic Syndrome
FILE REFERENCE: 21742 US1

CURRENT APPLICATION NUMBER: US/10/991,321

CURRENT FILING DATE: 2004-11-17

NUMBER OF SEQ ID NOS: 36

SOFTWARE: Patentin version 3.2

SEQ ID NO 23
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US-10-991-321-23
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TYPE: DNA
ORGANISM: Homo sapiens
US-10-991-321-23
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                                                                 GGTCCACAGAAAAGTATTTCTTTAATCTAAGTTCCATGACATGTGAAAAAATTCTTTTCCG
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           GTGGGTGTCACCGGAACCGGATTGAGAACAGGTTTCCAGATGAAGCTACTTGTATGGGCT
                                             GGTCCACAGAAAAGTATTTCTTTAATCTAAGTTCCATGACATGTGAAAAATTCTTTTTCCG
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Pred. No. 3.1e-247;
0; Mismatches 0;
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Sequence 19662, Application US/09814353

Publication No. US20030165831A1

REPLICANT: Lee, John
APPLICANT: Lilie, James
APPLICANT: Lilie, James
TITLE OP INVENTION: OVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OP INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OP INVENTION: THERAPY OF OVARIAN CANCER
FILE REPERENCE; MRI-006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/21,031
PRIOR PILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 60/21,940
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOPTMARE: FastERQ for Windows Version 4.0
SEQ ID NO 19662
LENGTH: 2407
TYPE: DNA
ORGANISM: Homo sapiens
US-09-814-353-19662
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US-09-814-353-19662
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                                       TTTATATATAACTAGCTGCTATTCAAATGTGAGTCTACCATTTTTAATTTTATGGTTCAAC 960
                                                                     TTGGTGATTTATTCACCAGTTTTTATTAATACAAGTCACTTTTTCAAAAATTTTGGATTTT
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Pred. No. 4.7e-247;
); Mismatches 0;
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RESULT 8
US-10-044-090-609
US-10-044-090-609

Sequence 609, Application US/10044090

Publication No. US20020137081A1

GENERAL INFORMATION:
APPLICANT: 01ga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN
FILE REFERENCE: PA-0028 US
CURRENT FILING DATE: 2002-01-09
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 609
LENGTH: 2540
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20020137081A1 1811
US-10-044-090-609
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Best Local Similarity
Matches 979; Conserv
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Sequence 143, Application US/10084817

| Publication No. US20030119009A1
| GENERAL INFORMATION:
| APPLICANT: SUSAN SEVENT:
| APPLICANT: SUSAN SEVENT:
| APPLICANT: SUSAN SEVENT:
| APPLICANT: Jacon M. Shohet
| TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
| APPLICANT: Jacon M. Shohet
| TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
| PILLE REFERENCE: PA-0046 US
| CURRENT APPLICATION NUMBER: US/10/084,817
| CURRENT FILING DATE: 2002-02-25
| PRIOR APPLICATION NUMBER: 60/270,784
| PRIOR PILING DATE: 2001-02-23
| NUMBER OF SEQ ID NOS: 365
| SOPTWARE: PERI PROGRAM
| SEQ ID NO 143
| LENGTH: 2540
| TYPE: DNA
| ORGANISM: Homo sapiens
| PEATURE:
| NAME/KEY: misc feature
| OTHER INFORMATION: Incyte ID No. US20030119009A1 181172CB1
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            CAACAGGAAATAACGCGGAGATCTGTCTCCTGCCCCTAGACTACGGACCCTGCCGGGCCC
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Sequence 315, Application US/10097340

Publication No. US20030087250A1

GENERAL INFORMATION:
APPLICANT: John MORAHAN
APPLICANT: Manjula GANNAVARAPU
APPLICANT: Sebastian HOERSCH
APPLICANT: Steve G. KOVATS
APPLICANT: Steve G. KOVATS
APPLICANT: Steve G. KOVATS
APPLICANT: Achel E. MEYERS
APPLICANT: Achel E. MEYERS
APPLICANT: Achel E. MEYERS
APPLICANT: Achel E. MEYERS
APPLICANT: COLANDT
APPLICANT: Cordon B. MILLS
APPLICANT: Robert C. BAST, Jr.
APPLICANT: Robert C. BAST, Jr.
APPLICANT: Robert C. BAST, Jr.
APPLICANT: Karen LIM
APPLICANT: Karen CHATT
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
FILE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
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US-10-097-340-315
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CURRENT FILING DATE: 2002-03-14

PRIOR APPLICATION NUMBER: 60/276,025

PRIOR APPLICATION NUMBER: 60/325,149

PRIOR APPLICATION NUMBER: 60/325,149

PRIOR APPLICATION NUMBER: 60/276,026

PRIOR PILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: 60/274,967

PRIOR PILING DATE: 2001/09/26

PRIOR PILING DATE: 2001-09-12

PRIOR PILING DATE: 2001-08-10

PRIOR RILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 60/325,102

PRIOR APPLICATION NUMBER: 60/323,580

PRIOR APPLICATION NUMBER: 60/323,580

PRIOR PILING DATE: 2001-09-19

VUMBER OF SEQ ID NOS: 363

SOFTWARE: FREESEQ FOR WINDOWS VETBION 4

SEQ ID NO 315

LENGTH: 1142

TYPE: DNA

OCALAR STATES

US-10-097-340-315
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Best Local Similarity 99.7%;
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US-10-021-660-53
; Sequence 53, Application US/10021660
; Publication No. US20030152926A1
; GENERAL INFORMATION:
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Best Local Similarity 99.7%;
Matches 974; Conservative
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APPLICANT: Glynne, Richard
APPLICANT: Watson, Susan R.
APPLICANTON: Modulators and Methods of Diagnosis of Angiogenesis
TITLE OF INVENTION: Modulators
TITLE OF INVENTION: Modulators
TITLE OF INVENTION: Modulators
CURRENT APPLICATION NUMBER: US/09/10/21,660
CURRENT APPLICATION NUMBER: US/09/784,356
PRIOR APPLICATION NUMBER: US/09/784,356
PRIOR APPLICATION NUMBER: US/09/784,356
PRIOR APPLICATION NUMBER: US/09/637,977
PRIOR FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 135
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Pred. No. 1.9e-245;
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Indels Length 1142;

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Sequence 23, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Afar, Natesha
APPLICANT: Ginberg, Wendy M.
APPLICANT: Ginberg, Wendy M.
APPLICANT: Ginb, Kurt C.
APPLICANT: Ginb, Kurt C.
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Mack, David H.
APPLICANT: Wateon, Susan R.
APPLICANT: Wateon, Susan R.
APPLICANT: Eos Biotechnology, Inc.
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APPLICANT: Wateon, Susan R.
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; ORGANISM: Homo sapiens
US-10-295-027-23
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NUMBER OF SEQ ID NOS: 1386
SOCTWARE: Patentin Ver. 2.1
SEQ ID NO 23
LENGTH: 1142
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OR APPLICATION NUMBER: US 60/335,394

OR FILING DATE: 2001-11-15

IOR APPLICATION NUMBER: US 60/332,464

IOR FILING DATE: 2001-11-21

OR APPLICATION NUMBER: US 60/334,393

IOR FILING DATE: 2001-12-14

IOR FILING DATE: 2001-12-14

IOR APPLICATION NUMBER: US 60/347,311

IOR FILING DATE: 2002-01-08

IOR APPLICATION NUMBER: US 60/347,349

IOR APPLICATION NUMBER: US 60/355,250

IOR APPLICATION NUMBER: US 60/355,250

IOR APPLICATION NUMBER: US 60/356,714

IOR FILING DATE: 2002-02-08

IOR APPLICATION NUMBER: US 60/356,714

IOR FILING DATE: 2002-02-08

IOR APPLICATION NUMBER: US 60/356,714

IOR FILING DATE: 2002-02-08

IOR APPLICATION NUMBER: US 60/356,714

IOR FILING DATE: 2002-02-08
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Local Similarity 99.7%;
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                                     ATACTGGCTGTGGAGGGAATGACAATAACTTTGTTAGCAGGGAGGATTGCAAACGTGCAT
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Pred. No. 1.9e-245;
0; Mismatches 3;
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Sequence 6, Application US/10428487

Publication No. US20040006780A1

GENERAL INFORMATION:
APPLICANT: RASTELLI, LUCA K.
APPLICANT: CERBER, HANS-PETER
TITLE OF INVENTION: VEGF-MODULATED GENES AND METHODS EMPLOYING THEM
PILE REPERENCE: 09800080-0103

CURRENT APPLICATION NUMBER: US/10/428,487

CURRENT APPLICATION NUMBER: 09/815,153

PRIOR APPLICATION NUMBER: 09/815,153

PRIOR APPLICATION NUMBER: 00/913,201

PRIOR APPLICATION NUMBER: 00/191,201

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Pred. No. 1.9e-245;
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                                                         APPLICANT: Murray, Richard
APPLICANT: Glynne, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators
FILE REFERENCE: 018501-006200US
CURRENT APPLICATION NUMBER: US 09/784,356
PRIOR APPLICATION NUMBER: US 09/784,356
PRIOR APPLICATION NUMBER: US 09/791,390
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/791,390
PRIOR APPLICATION NUMBER: US 60/310,025
PRIOR APPLICATION NUMBER: US 60/310,025
PRIOR APPLICATION NUMBER: US 60/310,025
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US-10-211-462-51
; Sequence 51, Application US/10211462
; Publication No. US20040033495A1
; GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: US 60/334,244 PRIOR FILING DATE: 2001-11-29 NUMBER OF SEQ ID NOS: 230
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 ATACTGGCTGTGGAGGGAATGACAATAACTTTGTTAGCAGGGAGGATTGCAAACGTGCAT
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APPLICANT: Wyeth

APPLICANT: Wounts, William

APPLICANT: Mounts, William

APPLICANT: Mounts, William

FITTLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

FILE REFERENCE: 031896-043000 (AM 101081)

CURRENT APPLICATION NUMBER: US$/10/956,157

CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SEQ ID NO 1625

SEQ ID NO 1625

SEQ ID NO 1625

TYPE: DNA

ORGANISM: Homo sapiens

US-10-956-157-1625
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US-10-956-157-1625

; Sequence 1625, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACGCCTTGCCCAGCGGGCCGCCCGACCCCTGCACCATGGACCCCGCTCGCCCCTGG
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CTGCCAATGTGACTCGCTATTATTTTAATCCAAGATACAGAACCTGTGATGCTTTCACCT
                       CTGCCAATGTGACTCGCTATTATTTTAATCCAAGATACAGAACCTGTGATGCTTTCACCT
                                                                                                       TCTGCGCACCAAAGAAAATTCCATCATTTTGCTACAGTCCAAAAGATGAGGGACTGTGCT
                                                                                                                                                             GTGGGTGTCACCGGAACCGGATTGAGAACAGGTTTCCAGATGAAGCTACTTGTATGGGCT
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                                                                                TCTGCGCACCAAAGAAATTCCATCATTTTGCTACAGTCCAAAAGATGAGGGACTGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 972.2; DB 9;
Pred. No. 1.9e-245;
0; Mismatches 3;
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	TGTTTGTGAGACTGAAT	, 961
978	TTTATATATAACTAGCTGCTATTCAAATGTGAGTCTACCATTTTTAATTTATGGTTCAAC	919
960	TTTATATATAACTAGCTGCTATTCAAATGTGAGTCTACCATTTTTAATTTATGGTTCAAC	, 901
918	TTGGTGATTTATTCACCAGTTTTTATTAATACAAGTCACTTTTTCAAAAATTTGGATTTT	859
900	TTGGTGATTTATTCACCAGTTTTTTTAATACAAGTCACTTTTTCAAAAATTTGGATTTT	, 841
858	GCTTATTTGCCTTTATGGTTGTATCTGAAGAATAATATGACAGCATGAGGAAACAAATCA	799
840		, 71
798	GGAAAATTCGGAAGAAGCAATTTTAAACATTCTTAATATGTCATCTTGTTTTGTCTTTATG	739
780	GGAAAATTCGGAAGAAGCAATTTTAAACATTCTTAATATGTCATCTTGTTTTGTCTTTATG	, 721
738	679 GTGCAAAAGCTTTGAAAAAAGAAAAAAGATGCCAAAGCTTCGCTTTGCCAGTAGAATCC	6
720	GTGCAAAAGCTTTGAAAAAAGAAAAAGAAGATGCCAAAGCTTTCGCTTTGCCAGTAGAATCC	, 661
678	619 ATACTGGCTGTGGAGGGAATGACAATAACTTTGTTAGCAGGGAGGATTGCAAACGTGCAT (6

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Search completed: March 11, 2006, 06:24:56 Job time: 992 secs

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                              4.6
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1: /cgn2 6/ptodata/2/pubpna/US08 NEW PUB.seq:*

2: /cgn2 6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /cgn2 6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

4: /cgn2 6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

5: /cgn2 6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

6: /cgn2 6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

7: /cgn2 6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

9: /cgn2 6/ptodata/2/pubpna/US11_NEW_PUB.seq:*

9: /cgn2 6/ptodata/2/pubpna/US11_NEW_PUB.seq:*

10: /cgn2 6/ptodata/2/pubpna/US11_NEW_PUB.seq:*

11: /cgn2 6/ptodata/2/pubpna/US11_NEW_PUB.seq2:*

12: /cgn2 6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*

13: /cgn2 6/ptodata/2/pubpna/US11_NEW_PUB.seq4:*

13: /cgn2 6/ptodata/2/pubpna/US11_NEW_PUB.seq4:*
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Match
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2 B US-10-310-914A-5835
2 B US-10-310-914A-5835
2 B US-10-310-914A-5873
3 B US-10-310-914A-5873
4 B US-11-137-465-14
8 US-11-137-506-2
12 US-11-1000-463-686
12 US-11-128-061-869
12 US-11-128-061-4511
12 US-11-128-049-451
12 US-11-128-049-6860
12 US-11-128-049-6860
12 US-11-128-049-6860
12 US-11-128-049-3218
12 US-11-128-049-3218
12 US-11-136-527-47
12 US-11-136-527-210
6 US-09-925-065A-164636
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(c) 1993 - 2006 Biocceleration Ltd.
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5168.979 Million cell updates/sec
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     Sequence 546, App
Sequence 5873, Ap
Sequence 14, Appl
Sequence 214, Appl
Sequence 214, Appl
Sequence 27, Appli
Sequence 286, App
Sequence 869, App
Sequence 4511, Ap
Sequence 4511, Ap
Sequence 4511, Ap
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Sequence 3218, Ap
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4.1 1	4.1	4.1	4.1	4.1	4.1	4.1	4.2	4.2	4.2	4.2	4.2	4.3	4.3	4.3	4.3	4.4	4.4	4.4	4.8	4.8	4.8	4.8	4.9	4.9
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Sequence 212, App	Sequence 45, Appl	Sequence 727350,	Sequence 436635,	Sequence 463534,	Sequence 463533,	Sequence 167190,	Sequence 15, Appl	Sequence 167189,	Sequence 167188,	Sequence 80, Appl	Sequence 78, Appl	43	Sequence 8627, Ap	Sequence 24917, A	Sequence 24917, A	Sequence 66413, A	Sequence 271, App	Sequence 289, App				Sequence 96, Appl	168,	Sequence 22, Appl

ALIGNMENTS

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Sequence 546, Application US/10821234

; Publication No. US20050255114A1

; GENERAL INFORMATION:

; APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR PILING DATE: 2003-04-07
; PRIOR FILING DATE: 2003-04-07
; ENGRE OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; ELECTH: 708
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; ORGANISM: Homo sapiens
US-10-821-234-546
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                              h 72.3%; Score 708; DB 8; L
Similarity 100.0%; Pred. No. 4.4e-151;
08; Conservative 0; Mismatches 0;
                                                                                                                    GACTACGGACCCTGCCGGGCCCTACTTCTCCGTTACTACTACGACAGGTACACGCAGAGAC
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                                                                                              GACTACGGACCCTGCCGGGCCCTACTTCTCCGTTACTACTACGACAGGTACACGCAGAGC
                           TGCCGCCAGTTCCTGTACGGGGGCTGCGAGGGCAACGCCAACAATTTCTACACCTGGGAG 278
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APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Uses thereof
FILE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 5835
LENGTH: 82
TYPE: RNA
ORGANISM: Human
US-10-310-914A-5835
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                                                                                                RESULT 3
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US-10-310-914A-5835
                            Sequence 5873, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5835, Application US/10310914A Publication No. US20060003322A1
APPLICANT: Bentwich, APPLICANT: Shiler, 1
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                                                                                                                                                                                                                                                                                        Match 8.4%; Score 82; DB 8; 1 Local Similarity 76.8%; Pred. No. 2.5e-09;
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 Shiler, Kvuzat
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US-10-310-914A-5873
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PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/192,158
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 60/192,668
PRIOR APPLICATION NUMBER: 60/200,166
PRIOR FILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: 60/200,166
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 66
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US-11-137-465-14
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APPLICANT: Murdoch, Paul R.
APPLICANT: Rizvi, Safia, K.
APPLICANT: Smith, Randall, F.
APPLICANT: Xiang, Zhaoying
APPLICANT: Kabnick, Karen
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof FILE REFERENCE: 06087.0200.CPUS01 CURRENT APPLICATION NUMBER: US/10/310,914A CURRENT FILING DATE: 2002-12-06 NUMBER OF SEQ ID NOS: 1388402 SOFTWARE: PatentIn version 3.3 SEQ ID NO 5873 LENGTH: 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 14
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CURRENT FILING DATE: 2005-05-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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Local Similarity 63.2%;
254 CGCCAACAATTTCTACACCTGGGAGGCTTGCGACGATGCTTGC 296
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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.

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Adi2	Adea	Ade80824	Abu07724	Aaw61535	Aaw30311	Aar78389	Aar92265	Aar92012	Ady58286	Ady36969	Adu73579	Adu06597	Adr1441	Adq88030	Adf09568	Aay49557	Aar81884	Aar67994	Abr48478	Abr48476
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ALIGNMENTS

RESULT 1 ARAR74977 ID ARAR74977 ID ARAR7497 AC ARAR7497 AC ARAR7497 AC ARAR74 AC ARAR7 AAR74977 standard; protein; 235 Human Kunitz-type protease-inhibitor TFPI-2. 21-JAN-1996 AAR74977; Sprecher CA, 05-NOV-1993; 02-NOV-1994; 11-MAY-1995 WO9512674-A1 Homo anticoagulant; Kunitz-type inhibitor; protease-inhibitor; enzyme-inhibitor; (ZYMO) ZYMOGENBTICS INC. (UYNE-) UNIV NEW MEXICO STATE. sapiens. (first Kisiel W, deep vein thrombosis. 93US-00147710. 94WO-US012609. entry) Foster DC; Š

KTI is used to inhibit blood coagulation in mammals. It is particularly used as an anticoagulant and in the treatment of deep vein thrombosis, disseminated intravascular coagulations, pulmonary embolism and in the prevention of thrombosis following surgery. KTI inhibits Factor-VIIa in the absence of Factor-Xa, and thus does not require production of Factor-Xa via the intrinsic or extrinsic pathway. This KTI protein shares AA sequence homology and overall domain organization with tissue factor sequence homology and overall domain organization with tissue factor

Sequence 235 AA;

pathway-inhibitor (TFPI), and

has therefore been designated TFPI-2

Human Kunitz-type protease inhibitors - treatment of deep vein thrombosis.

used

as anticoagulants and in the

Claim

2; Page 50; 65pp; English.

WPI; 1995-193821/25. N-PSDB; AAQ90469.

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 have cytostatic activity and can be used in gene therapy, antisense inhibition and in vaccines. The NAs and the lung tumour-associated proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with their inappropriate expression, especially lung cancers. For example, the NAs may be administered to treat diseases by rectifying mutations or deletions in a patient's general content.
                                                                             The present invention describes immunogenic portions of lung tumourassociated proteins (I) and the nucleic acids (NAs) that encode them.
                                                                                                                                         Lung tumor-associated proteins and the nucleic acids that encode them useful for preventing, diagnosing and treating lung cancer.
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22-MAR-2000;
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27-APR-2000;
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17-DEC-1999;
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                                                                                                                  Page 260-261; 436pp; English.
                                                                                                                                                                                                                                                                       99US-00476300.

2000US-00519642.

2000US-00533077.

2000US-0054659.

2000US-00560406.

2000US-00589184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer; lung tumour; lung tumour protein; gene therapy;
antigen; lung tumour-specific antigen; diagnosis; vaccine;
antisense inhibition.
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99US-00466867.
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that affect the activity of the protein by expressing inactive proteins or to supplement the patients own production of (1). Additionally, the NAs may be used to produce the lung-tumour associated protein, according to standard recombinant DNA methodology. Conversely, antisense NA molecules may be administered to down regulate protein expression. The NA and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar NA sequences in samples, and hence which patients may be in need of treatment for lung cancer. The (1) may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of the protein. ARF68083 to ARF6878 and ARF76848 to ARF76878 represent human lung tumour protein related nucleotide and protein sequences which are used in the exemplification of the present expression and extinct and antagonists antagonists and antagonists and antagonists and antagonists and antag
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                 RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKKKMPKLRFASRIRKIRKKQF
                                                                          TCEKFFSGGCHRNRI ENRFPDEATCMGFCAPKKI PSFCYSPKDEGLCSANVTRYYFNPRY
                                                                                                                                     CRQFLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSM
                                                                                                                                                                            MDPARFIGLSI LLLFLTEAALGDAAQEFTGNNAEI CLLFLDYGFCRALLLLRYYYDRYTQS
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                                                                                                                   CROFLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSM
RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKKMPKLRFASRIRKIRKKQF
                                                           TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIPSFCYSPKDEGLCSANVTRYYFNPRY
                                                                                                                                                                                                                                      100.0%; Score 1306; DB 4; ilarity 100.0%; Pred. No. 4.5e-114; Conservative 0; Mismatches 0;
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ABG96429;
               ABG96429
               standard;
              protein;
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Human ovarian cancer marker M588.

11-DEC-2002

(first

entry)

RESULT 3
ABG9619
ID ABG9
XX ABG9
XX ABG9
XX ABG9
XX XX Huma
XX Huma
XX Huma
XX Honot
XX Homo
X Human; ovarian cancer; marker; cancer; familial history; brain disorder; central nervous system disorder; bacterial meningitis; viral meningitis; Alzheimer's disease; Parkinson's disease; cerebral oedema, hydrocephalus; brain herniation; inflammation; encephalitis; testicular disorder; nontuberculous granulomatous orchitis; connective tissue disorder; heart disorder; schaemic heart disorder; heart disorder; heart disorder; orchitis; connective tissue disorder; heart disorder; testicular disorder; orchitis; connective tissue disorder; heart disorder; neoplasm;

sapiens.

14-MAR-2001; 14-MAR-2001; 10-AUG-2001; 19-SEP-2001; 26-SEP-2001; 26-SEP-2001; 26-SEP-2001; 14-MAR-2002; ; 2001US-0276025P. ; 2001US-0276026P. ; 2001US-0311732P. ; 2001US-0323580P. ; 2001US-0324967P. ; 2001US-0325102P. 2002WO-US007826.

2001US-0325149P

(MILL-) MILLENNIUM PHARM INC

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AC AAU8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders (e.g. cerebral oedema, hydrocephalus or brain herniations), inflammations (e.g. bacterial or viral meningitis or encephalitis), testicular disorders (e.g. nontuberculous granulomatous orchitis), connective tissue disorders, or heart disorders (e.g. ischaemic heart disease or atherosclerosis). The compositions and methods may also be used in assessing the histological type of neoplasm associated with ovarian cancer, monitoring the progression of ovarian cancer, determining whether ovarian cancer has metastasized or is likely to metastasize, selecting a composition for inhibiting ovarian cancer, assessing the ovarian carcinogenic potential of a compound, or inhibiting ovarian cancer or at risk of developing ovarian cancer. The present amino acid sequence represents one of the ovarian cancer markers described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a new method for assessing whether a patient is afflicted with ovarian cancer. The method involves comparing the expression level of a marker in a patient sample and the normal level of expression of the marker in a control non-ovarian cancer sample, where the marker is selected from 363 cancer markers described in the specification. The method of the invention is useful in diagnosing or characterising cancer, in detecting the presence of cancer as early as possible, and the recurrence of ovarian cancer. The method may also be of particular use with patients having an enhanced risk of developing ovarian cancer (e.g. patients having a familial history of ovarian cancer). The cancer markers may be used in the management and treatment of e.g. brain and central nervous system disorders (e.g. bacterial and viral meningitis, Alzhaimer's disease or Parkinson's disease), brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monahan JB, Garman, RB, Morrisey MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assessing whether a patient is afflicted with ovarian cancer, useful in assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and
                                                                                AAU85511 standard,
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                                        AAU85511;
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                                                                                                                                                                                  RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKMPKLRFASRIRKIRKKQF 235
                                                                                                                                                                                                            RTCDAPTYTGCGGNDNNFVSREDCKRACAKALKKKKXXMPKLRFASRIRKIRKKQF
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Morrisey MP, Olandt PJ, Sen A, Vieby PO,
K, Schmandt RE, Zhao X, Glatt K;
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  (first entry)
                                                                                protein,
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D, Mills GB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-SEP-2000;
26-SEP-2000;
06-OCT-2000;
                                                                                                                                                                                                                                                                                             Sequence 235 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polynucleotide encoding a lung tumor polypeptide useful for stimulating and/or expanding T cells specific for a tumor protein
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N-PSDB; ABK38057.
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13-DEC-2000;
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29-AUG-2000;
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                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                         MDPARPLGLSILLLFLTEAALGDAAQEPTGNNAEICLLPLDYGPCRALLLRYYYDRYTQS
                                                                                                                                                                                            MDPARPLGLSILLLETTEAALGDAAQEPTGNNAEICLLFLDYGFCRALLLRYYYDRYTQS
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                  RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKMPKLRFASRIRKIRKKQF 235
                                                                                                                  CROFLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSM 120
                                                       TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIPSFCYSPKDEGLCSANVTRYYFNPRY
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); 2000US-00671335.

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); 2000US-00736457.

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Pred. No. 4
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PR 21-1
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                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated polynucleotide (I) comprising: (a) CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b) CC complements of (a); (c) sequences consisting of at least 20 contiguous CC residues of (a); (d) sequences that hybridize to (a), under moderately CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP86596-CC ABP86637) encoded by (I) and oligonucleotide can be used to detect cancer in a patient and compositions comprising polypeptides, polynucleotides, CC antibodies, fusion proteins, T cell populations and antigen presenting CC cells expressing the polypeptide are useful in treating pancreatic cancer CC and stimulating an immune response. The polynucleotides can be used as CC probes or primers for nucleic acid hybridisation, in the design and CC preparation of ribozyme molecules for inhibiting expression of the tumour CC polypeptides and proteins in the tumour cells, in vaccines and for gene CC therapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
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09-FEB-2001;
21-MAR-2001;
28-APR-2001;
16-MAY-2001;
12-JUL-2001;
20-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and pancreatic tumor polypeptides, useful for diagnosing, preventing and/or treating cancer, particularly pancreatic
                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; SEQ ID NO 167; 300pp + Sequence Listing; English
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N-PSDB; ABV94764.
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CRQFLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSM
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1, 2001US-0265682P.
1, 2001US-0267568P.
1, 2001US-0278651P.
1, 2001US-0287112P.
1, 2001US-0291631P.
1, 2001US-0305484P.
1, 2001US-0313999P.
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                                                                                                                                                                                             Score 1306; DB 5;
Pred. No. 4.5e-114;
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RESULT 6
ABU03481
ID ABU0
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                                                The present invention relates to methods and compositions for detecting CC an angiogenesis-associated transcript in a cell in a patient. The method CC involves contacting a biological sample from the patient with a CC involves contacting a biological sample from the patient with a CC polynucleotide that selectively hybridises to a sequence at least 80% CC identical to any of the angiogenesis-associated human polynucleotide sequences comprise genes that exhibit changes in CC expression levels as a function of time in tissue undergoing angiogenesis. The method and the polynucleotide sequences of the CC angiogenesis-associated diseases e.g. cancer. The polynucleotide requences are useful for disgnosing and treating angiogenesis and CC angiogenesis-associated diseases e.g. cancer. The polynucleotide sequences are useful as a vaccine for therapeutic and prophylactic immunisation.

CC ABU03456-ABU03569 represent angiogenesis-associated protein sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-FEB-2001;
22-FEB-2001;
19-APR-2001;
03-AUG-2001;
   Sequence 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting angiogenesis-associated transcript in a cell for diagnosing treating cancer by contacting a sample with a polynucleotide that exhibits changes in expression level as a function of time in tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  undergoing anglogenesis.
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29-NOV-2001;
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; 2001US-0334244P.
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Query Match Best Local Similarity

100.0%;

Score Pred.

1306; DB 6; No. 4.5e-114;

Length 235

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RESULT 7
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10-MAY-2001;
09-NOV-2001;
The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lung cancer-associated polypeptide; cytostatic; emphysema; atelectasis antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis small cell lung cancer; benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
                                                                                                                                                                                                                                                                                                                                                        Detecting a lung cancer-associated transcript in a cell from a pat: for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.
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29-NOV-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aziz N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lung cancer-associated polypeptide #192
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DB; ABX76328.
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                                                                                                                                                                                                                                                                                                 27; Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; protein; 235
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; 2001US-0339245P.
; 2001US-0350666P.
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Clapper JD;
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                                                                WPI; 2003-352750/33.
N-PSDB; ACA10386.
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Novel lung cancer polynucleotide encoding lung cancer protein, useful for detecting the presence of lung cancer in a patient, and in pharmaceutical

e.g. vaccines, for treating lung cancer

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RESULT 9
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                          ABU66385
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                        protein; 235 AA
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                                                                                                                                                                                                                           Sequence 235
                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 332; 82pp; English.
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26-SEP-2000;
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27-APR-2000;
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22-MAR-2000;
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15-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                        New polynucleotide, useful for preparing a cinhibiting development of cancer, e.g. lung
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-328427/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lung cancer therapyand diagnosis associated protein #9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU66385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-DEC-1999;
                                                                                                                                                                               235;
             181
                                    121
                                                          121
                                                                                  61
                                                                                                         61
                                                                                                                                             1 MDPARPIGLSILLLPLTEAALGDAAQEPTGNNABICLLPLDYGPCRALLLRYYYDRYTQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORIXA CORP.
                                                                                                   CRQFLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSM
RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKMPKLRFASRIRKIRKKQF
                                                       TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIPSFCYSPKDEGLCSANVTRYYFNPRY
                                                                                  CRQFLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSM
                                                                                                                                MDPARPLGLSILLLFLTEAALGDAAQEPTGNNAEICLLFLDYGPCRALLLRYYYDRYTQS
                                    TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIPSFCYSPKDEGLCSANVTRYYFNPRY
                                                                                                                                                                                                                                                                                                                                                                                                                 Carter D,
                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-00519642.
2000US-00546259.
2000US-00546259.
2000US-00560406.
2000US-00589184.
2000US-00651851.
2000US-00651854.
2000US-00651824.
2000US-006774125.
2000US-006774125.
2000US-00677415.
2000US-00736457.
                                                                                                                                                                                                                           B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001US-00902941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic; vaccine; gene therapy; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001US-00849626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-00346492
99US-00419356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-00466867.
                                                                                                                                                                                                                                                                                                                                                                                                                             H
                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                  Watanabe
Fanger GR,
                                                                                                                                                                                         Score 1306; DB 6;
Pred. No. 4.5e-114;
                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 Y, Johnson JC, Retter
Vedvick TS, Bangur CS
                                                                                                                                                                                                                                                                                                                                                                   composition
                                                                                                                                                                                                                                                                                                                                                           cancer.
                                                                                                                                                                              0,
                                                                                                                                                                                                   Length
                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                      for
                                                                                                                                                                                                                                                                                                                                                                                                                              MW;
                                                                                                                                                                                                     235;
                                                                                                                                                                                                                                                                                                                                                                    treating
                                                                                                                                                                                                                                                                                                                                                                                                                  Mcnabb
                                                                                                                                                                              0
                                                                                                                                                                            Сарв
             235
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Best+Local Similarity
Matches 235; Conserv
                                                                                                                                                                                                                                                                                                                                  The invention relates to novel compositions and methods for the therapy and diagnosis of cancer, particularly lung cancer. The compositions comprise one or more lung tumour polypeptides, immunogenic portions therof, polynuclectides that encode such polypeptides, antigen presenting cells that express such polypeptides, and T cells that are specific for cells expressing such polypeptides, and Tells that are specific for cytostatic and immunostimulant activity. The lung tumour antigens can be used in the creation of a vaccine. The polynuclectides that encode the lung tumour selfunds can be used in gene therapy to help in the creatment of lung tumours. This sequence represents a human lung tumour clone polypeptide of the invention. This sequence was not shown in the specification. It has been taken from a World Intellectual Property
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptides and encoding polynucleotides, useful for diagnosing, preventing and/or treating lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bangur CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human lung tumour clone protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADH45851 standard; protein; 235 AA.
                                                                                                                                                                                                                                                                                        Sequence 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1, SEQ ID NO 332; 258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-468346/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Johnson JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Henderson RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-OCT-2001; 2001US-00017754
28-MAR-2002; 2002US-00113872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-OCT-2002; 2002WO-US034777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            numan; clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADH45851,
                                                                                                                                                                                                                                                                                                                        Organization CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ung cancer; tumour; cytostatic; immunostimulant; vaccine; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                 121
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                                                                                                                                                                                  MDPARPLGLSILLLFLTEAALGDAAQEPTGNNAEICLLFLDYGFCRALLLRYYYDRYTQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKMPKLRFASRIRKIRKKQF 235
                                                                                               CROPLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSM
RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKMPKLRFASRIRKIRKKQF 235
                                 TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIPSFCYSPKDEGLCSANVTRYYFNPRY
                                                   TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIPSFCYSPKDEGLCSANVTRYYFNPRY
                                                                                                                    CRQFLYGGCEGNANNFYTWEACDDACWRIEKVFKVCRLQVSVDDQCEGSTEKYFFNLSSM
                                                                                                                                                              MDPARPLGLSILLLFLTEAALGDAAQEPTGNNAEICLLPLDYGPCRALLLRYYYDRYTQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mcnabb A;
                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                          8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                          ROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treating
                                                                                                                                                                                                                                                                                                                        supplied with the specification.
                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Watanabe Y,
Durham M,
                                                                                                                                                                                                                          Score 1306; DB 7;
Pred. No. 4.5e-114;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID No 332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kalos MD,
Carter D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fanger GR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sleath
                                                                                                                                                                                                                                                        Length 235;
                                                                                                                                                                                                                            Indels
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                                                               180
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  181 RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKMPKLRFASRIRKIRKKQF
    235
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Human apoptosis-associated protein SEQ 08-SEP-2005 22-APR-2004 ADI62727; ADI62727 standard; protein; (revised)
(first entry) 235 ID 170.

autoimmune disease; degenerative disease; viral infection; leukaemia; carcinoma; sarcoma; multiple sclerosis; rheumatoid arthritis; diabetes; lupus; hepatitis; influenza viruses; Alzheimer's disease; Huntington's disease; Parkinson's diseases; reperfusion injury; stroke; alcoholic liver disease; human. antirheumatic; antiarthritic; dermatological; antiinflammatory; hepatotropic; virucide; nootropic; anticonvulsant; antiparkinsonian; vasotropic; cerebroprotective; antialcoholic; gene therapy; tumour; vasotropic; derbroprotective; antialcoholic; gene therapy; tumour; apoptosis; cell death; cytostatic; neuroprotective; immunosuppressive;

Homo sapiens.

WO2003058021-A2

17-JUL-2003

13-JAN-2003; 2003WO-EP000270.

11-JAN-2002; 2002DE-01000856.

(XANT-) XANTOS BIOMEDICINE AG

Koenig-Hoffman K, Kazinski M, Schaefer R, Kesper

New nucleic acids involved in apoptosis, useful for diagnosis and treatment of e.g. tumors and degenerative disease, also related p of e.g. tumors and modulators. related proteins,

Claim 1a; SEQ ID NO 170; 517pp; German.

AD1627 AD1627 XX AD162 XX AD162 XX OB-SE DT 08-SE DT 22-AP XX Human XX Human XX Autoi XX Lopat XX Lopat XX Lopat XX Human XX Human XX Human XX Human XX Homo XX WO200 XX 17-JU XX I7-JU X with hepatitis or influenza viruses, and environment of genetities are derived from a normalised compositie measured by cell death detection assay or the CPRG assay composities measured by cell death detection assay or the CPRG assay composities measured by cell death detection assay or the CPRG assay composities of the invention and the extent of the ave cytostatic, neuroprotective, immunosuppressive, antirheumatic, compositive, anticonvulsant, antiparkinsonian, vasotropic, virucide, compositive, anticonvulsant, antiparkinsonian, vasotropic, virucide, compositive, anticonvulsant, antiparkinsonian, vasotropic, compositive, antiparkinsonian, vasotropic, compositive, compositive, compositive, antiparkinsonian, vasotropic, compositive, compositive, antiparkinsonian, vasotropic, virucide, compositive, antiparkinsonian, carcinoma, sarcoma, compositive, c invention describes novel nucleic acid molecules that are associated a normalised the extent of an

Revised record issued ဓ္ဌ 08-SEP-2005 : Revision to cross-reference field

Sequence 235 AA

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                             03-DEC-2001;
14-DEC-2001;
08-JAN-2002;
10-JAN-2002;
08-FEB-2002;
13-FEB-2002;
20-FEB-2002;
29-MAR-2002;
04-APR-2002;
15-JUN-2002;
16-JUL-2002;
                                                                                                                                                                                                                                                                     13-NOV-2001;
21-NOV-2001;
29-NOV-2001;
 N-PSDB;
  WPI; 2003-468649/44.
N-PSDB; ADN38705.
                                                                                                                                                                                                                                                                                                                     13-NOV-2002;
                                                                                                                                                                                                                                                                                                                                                                   WO2003042661-A2
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                      detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; differential expression; cancer; angiogenic disorder; fibrotic disorder; psoriasis; ischaemia; heart disease; atheros inflammatory disease; autoimmune disease; retinal neovascularistaion syndrome; scarring; uterine fibroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:24.
                                                                                                                                                                                                                                                                                                                                                                                                              vulnerary; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADN38706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADN38706 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                             healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MDPARPLGLSILLLFUTEAALGDAAQEPTGNNAEICLLFLDYGFCRALLLRYYYDRYTQS
                                                                       SOB
                                Aziz N, Gir
Murray R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCEKFFSGGCHRNRIENRFPDEATCMGFCAFKXIPSFCYSPKDEGLCSANVTRYYFNFRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CROFLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKMPKLRFASRIRKIRKKQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKMPKLRFASRIRKIRKKQF 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIPSFCYSPKDEGLCSANVTRYYFNPRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRQFLYGGCEGNANNFYTWEACDDACWRIEKVFKVCRLQVSVDDQCEGSTEKYFFNLSSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MDPARPLGLS ILLLELTEAALGDAAQEPTGNNAEICLLELDYGPCRALLLRYYYDRYTQS
                                                                                                                                                                                                                                                                                                                                                                                                                       dlagnosis; prognosis; drug screening; drug targeting;
ing; contraception; cytostatic; cardiant; immunomodulatory;
                                                                                        2001US-0332464P.
2001US-034339P.
2001US-0340376P.
2002US-0347311P.
2002US-0355250P.
2002US-0355907P.
2002US-0355907P.
2002US-036807P.
2002US-0370110P.
2002US-0370110P.
2002US-03977246P.
2002US-03977246P.
2002US-03977246P.
2002US-03977246P.
2002US-03977246P.
2002US-03977246P.
2002US-03977246P.
2002US-03977246P.
2002US-03977246P.
2002US-039773P.
                                                                    BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                     2002WO-US036810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                               therapy; vaccine.
                                             Ginsburg WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1306; DB 7;
100.0%; Pred. No. 4.5e-114;
                                   SR,
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                                  Gish KC, G
Wilson KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
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                                Glynne R,
E, Zlotnik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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                                Hevezi PA; c A;
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XFFFXXX555555555555555555555555555
                                                                                                                                                       Determining the presence or absence of a pathological useful for diagnosing, prognosing or treating cancer, a nucleic acid in a biological sample.
                                                                                                                                                              cell in a patient, comprises detecting
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Claim 12; SEQ ID NO 24; 1385pp; English.

cc whose expression is upregulated or downregulated in specific cancers or cother diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a cc patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The cc invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; antibodies which specifically bind a cc polypeptide of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and mucleic acids. The nucleic acids, polypeptides, and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, atherosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularistation syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present of sequence represents a polypeptide of the invention. The invention relates to nucleic acids and proteins (ADN38683-ADN40064)

Sequence 235 AA;

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Best Local Simi:
Matches 235;
                                                                                                                                                                                                                      Local Similarity
   181
                          181
                                                   121
                                                                             121
                                                                                                     61
                                                                                                                              13
                                                                                                                                                        μ
RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKMPKLRFASRIRKIRKKQF
               RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKMPKLRFASRIRKIRKKQF 235
                                                 TCEKFFSGGCHRNTENRFPDEATCMGFCAPKKIPSFCYSPKDEGLCSANVTRYYFNPRY
                                                                                                  CRQFLYGGCEGNANNFYTWEACDDACWRIEKVEKVCRLQVSVDDQCEGSTEKYFFNLSSM
                                                                                                                  CRQFLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSM
                                                                                                                                                   MDPARPLGLS ILLLELTBAALGDAAQBPTGNNABICLLPLDYGPCRALLLRYYYDRYTQS
                                                                                                                                                                    MDPARPLGLSILLLFLTEAALGDAAQEPTGNNABICLLFLDYGPCRALLLRYYYDRYTQS
                                                                          TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIPSFCYSPKDEGLCSANVTRYYFNPRY 180
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                       0,
                                                                                                                                                                                                                    Score 1306;
Pred. No. 4.
                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                    4.5e-114;
                                                                                                                                                                                                                              DB 7; Length
                                                                                                                                                                                                       0
                                                                                                                                                                                                       Indels
                                                                                                                                                                                                       0
                                                                                                                                                                                                      Gaps
 235
                                                                                                                           120
                                                                                                   120
                                                                                                                                                    60
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RESULT 13
ADE71603
ID ADE71
XX ADE71
XX ADE71
XX ADE71
XX Puman
XX Human
XX Human
XX Homo
XX Homo
XX US200
PN US200
PN US200
PPF 30-JU
PF 30-JU
PR 15-OC
PR 17-DE
XX (WANG
                    30-JUN-1999;
15-OCT-1999;
17-DEC-1999;
                                                                                                                                                                                                                           ADB71603 standard; protein; 235 AA
                                                             30-DEC-1999;
                                                                                 03-JUL-2003
                                                                                                    US2003125245-A1
                                                                                                                        Homo gapiens.
                                                                                                                                              human;
                                                                                                                                                                Human lung tumour protein #9.
                                                                                                                                                                                      29-JAN-2004
                                                                                                                                                                                                         ADE71603;
 (WANG/) WANG
                                                                                                                                           lung
                                                                                                                                             tumour;
                                                                                                                                                                                     (first entry
                   99US-00346492.
99US-00419356.
99US-00466867.
                                                             99US-00476300
                                                                                                                                           cancer; lung cancer; vaccine
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BANGUR C 8

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RESULT 14
ADL83255
ID ADL83
XX ADL83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a polypeptide comprising at least an immunogenic portion of a lung tumour protein or variant. The invention is useful for chihibiting the development of a cancer, particularly lung cancer, in a patient by administering to a patient an effective amount of a cancer, particularly lung cancer, in a patient by administering to a patient an effective amount of a compensation of the polypeptide, an effective amount of an antibody or antityen-binding fragment an antigen-presenting cell that expresses a polypeptide where the antigen-presenting cell is a dendritic cell, a biological sample treated by a method of the invention or an isolated T cell population prepared by a method of the invention. The pharmaceutical compositions and vaccines of the invention are also used for inhibiting the development of cancer. Methods are also provided for diagnosing cancer and also monitoring the progression of cancer. Current therapies of cancer are based on the combination of chemotherapy or suggery or radiation which prove to be inadequate in many patients. This invention provides effective vaccines and compositions which may be used in therapy. The compositions also provide early diagnostic procedures. The present sequence represents the amino acid sequence of a bursen lung times.
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Best Local !
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                                                                                                                                                                    Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic; Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory; Gene Therapy; PRO; B cell related disorder; cancer;
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                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                   Human PRO35972, SEQ ID 457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADL83255
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                                                                                                                                           immune-mediated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 100.0%; Score 1306; DB 8; Similarity 100.0%; Pred. No. 4.5e-114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIPSFCYSPKDEGLCSANVTRYYFNPRY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRQPLYGGCEGNANNPYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGGTEKYPFNLSSM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKKMPKLRFASRIRKIRKKQF 235
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WO2004024097-A2

lung tumour;

cytostatic; lung cancer; human.

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RESULT 15
ADJ19770
ID ADJ15
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                          Human lung cancer-related protein - SEQ ID 332
                                                                                                                                                                                                                                                                                                                       Sequence 235 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New PRO polypeptide, useful for diagnosing and treating a B cell related disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
                                              04-NOV-2004
                                                                ADJ19770;
                                                                                 ADJ19770 standard; protein; 235 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-SEP-2002; 2002US-0411392P
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                                              (first entry
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Pred. No. 4.5e-114;
); Mismatches 0;
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US2003211510-A1

Homo sapiens

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Best Local S
Matches 235
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11-JUL-2000;
29-AUG-20000;
08-SEP-2000;
26-SEP-2000;
06-CCT-20000;
30-CCT-20000;
13-DEC-2000;
03-MAY-2001;
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06-MAR-2000;
22-MAR-2000;
10-APR-2000;
27-APR-2000;
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15-OCT-1999;
17-DEC-1999;
                                                                                                                                                                                                                 The invention relates to a novel isolated polynucleotide comprising a sequence chosen from any one of 40 lung tumour polypeptides or its complements, fragments or degenerate variants. The method of the invention has cycostatic applications and may be useful for detecting and treating lung cancer in a patient via incubating CD4+ and/or CD8+ T cells isolated from a patient with at least one component chosen from a polypeptide, polynucleotide or antigen presenting cell (APC) of the invention and administering an effective amount of the proliferated T cells to the patient. The current sequence is that of the human lung cancer-related protein of the invention. The current sequence is not shown in the specification per se but is available on the USPTO web-site http:seqdata.uspto.gov/sequence.html?DocID=20030211510.
                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polynucleotide encoding lung tumor polypeptides, useful for diagnosing, preventing and treating cancer e.g. lung cancer.
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Johnson JC, Retter MW,
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DB; ADJ19502.
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235; Conserv
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TCEKFFSGGCHRNRIENRFFDEATCMGFCAFKKIPSFCYSFKDEGLCSANVTRYYFNPRY 180
                                        CROPLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSM
                                                        CRQFLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSM
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2000US-0053967.
2000US-00546259.
2000US-00589184.
2000US-00614124.
2000US-006581563.
2000US-00658824.
2000US-00671325.
2000US-00671325.
2000US-00671419.
2000US-00702705.
2000US-00849626.
2001US-000175941.
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99US-00419356.
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Durham M,
                                                                                                                                         Score 1306; DB 8;
Pred. No. 4.5e-114;
); Mismatches 0;
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Carter D,
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S 문 181 RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKKMPKLRFASRIRKIRKKQF 235 121 TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIPSFCYSPKDEGLCSANVTRYYFNPRY 180

RTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKKKMPKLRFASRIRKIRKKQF 235

Search completed: March Job time : 192 BecB time : 192 весв 9, 2006, 19:52:52

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1185 CGGCAACAACTTCCACAGCCGCGAGAGCTGCGAGGATGCCTGC 1227

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APPLICANT: Chen, Rui-hong
APPLICANT: Wang, Zhiwei
APPLICANT: Wentman, Tom
APPLICANT: Wentman, Tom
APPLICANT: Zhang, Jie
APPLICANT: Cao, Yi-Cheng
APPLICANT: Chou, Ping
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILS REFERENCE: 785CIP4CN
CURRENT APPLICATION NUMBER: US/11/000,463
CURRENT APPLICATION NUMBER: 10/291,265
PRIOR APPLICATION UNUMBER: 10/291,265
PRIOR FILING DATE: 2002-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; SEQ ID NO 688
LENGTH: 915
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-688
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                                                                                                                                                                                                                                                                           APPLICANT: Tang, Y Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Chen, Rui-hong
APPLICANT: Qian, Xiaohong
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Sequence 688, A
Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.0%;
Best Local Similarity 52.7%;
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 214, Application US/11000463 Publication No. US20050266423A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOPTMARE: pt SEQ_genes Version 1.0
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APPLICANT: Stache
APPLICANT: Andart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 821A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               560 TTATTTTAATCCAAGATACAGAACCTGTGATGCTTTCACCTATACTGGCTGTGGAGGGAA 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     500 TCCATCATTTTGCTACAGTCCAAAAGATGAGGGACTGTGCTCTGCCAATGTGACTCGCTA 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            680 GAAAAAGAAGATGCCAAAGCTTCGCTTTGCCAGTAGAATCCGGAAAAATTCGGAAGAAGCA 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 620 TGACAATAACTTTGTTAGCAGGGAGGATTGCAAACGTGCATGTGCAAAAGCTTTGAAAAA 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATT 742
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Tang, Y. Tom
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Pred. No. 0.00097;
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Matches

135 GCGGAGATCTGTCTCCTGCCCCTAGACTACGGACCCTGCCGGGCCCTACTTCTCCGTTAC 194

Score 56.8; DB 9; Pred. No. 0.0036; 0; Mismatches 67;

Length 1413;

0;

Query Match 5.8%; Best Local Similarity 59.1%;

(227) ... (1285)

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APPLICANT: Beyer, Wayne F.
APPLICANT: Venetta, Thomas M.
APPLICANT: Venetta, Thomas M.
APPLICANT: Scroelke, John W.
APPLICANT: Blaesius, Rainer H.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE FILE REPERENCE: 46143/294851
CURRENT APPLICATION NUMBER: US/11/177,506
CURRENT FILING DATE: 2005-07-08
PRIOR APPLICATION NUMBER: 60/586,856
PRIOR APPLICATION NUMBER: 60/586,856
PRIOR FILING DATE: 2004-07-09
NUMBER OF SEQ ID NOS: 52
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
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PRIOR PILING DATE: 2001-01-25;
PRIOR PPLICATION NUMBER: 09/922,279
PRIOR PILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR PILING DATE: 2000-01-25;
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR PILING DATE: 2000-07-17
PRIOR PILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR APPLICATION NUMBER: 09/633,870
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-09-15
PRIOR PILING DATE: 2000-09-15
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; NAME/KBY: CDS
; LOCATION: (22:
US-11-177-506-2
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Publication No. US20060029956A1
GENERAL INFORMATION:
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                  ORGANISM: Homo FEATURE:
                                                                                                                     TYPE: DNA
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LOCATION: (103)..(1158)
                                                                                                                                         ENGTH: 1413
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Pred. No. 0.0035;
0; Mismatches 67;
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APPLICANT: Zhou, Ping
APPLICANT: Cao, Yi-Cheng
APPLICANT: Drmanac, Radoje T.
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 785CIP4CN
CURRENT APPLICATION NUMBER: US/11/000,463
CURRENT FILING DATE: 2004-11-29
PRIOR APPLICATION NUMBER: 10/291,265
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR PILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR APPLICATION NUMBER: 09/922,279
PRIOR APPLICATION NUMBER: 09/922,279
PRIOR PILING DATE: 2001-08-03
                 RESULT 9
US-11-128-061-869
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US-11-000-463-686
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Sequence 869, Application US/11128061
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Best Local Similarity 59.1%;
Matches 97; Conservative
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SEQ ID NO 686
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APPLICANT:
APPLICANT:
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PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 09/633,870
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PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR FILING DATE: 2000-07-17
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APPLICANT: Liu, Chenghua
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                                                                                                      GGGAACAAGTTCTACTCAGAGAAGGAGTGCAGAGAGTACTGCGG 1300
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Qian, Xiaohong B.
Wang, Zhiwei
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o. US20050266423A1
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                                                                                                                                                                                                                                                                                                                                                              Score 56.8; DB 12;
Pred. No. 0.0036;
0; Mismatches 67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-11-128-061-4511
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                                                                                   SOFTWARE: PatentIn version 3.3 SEQ ID NO 4511
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APPLICANT:
APPLICANT:
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LENGTH: 1234
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Best Local 9
                                                                                                                           APPLICANT: Brown, Eugene L.
APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
FILE REFERENCE: 01997.027701
CURRENT APPLICATION NUMBER: US/11/128,061
CURRENT FILING DATE: 2005-05-11
CURRENT FILING DATE: 2005-05-11
PRIOR FILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
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APPLICANT: Miller, Christopher P.
TITLE OP INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
TITLE OP INVENTION: TO MONITOR GENE EXPRESSION
FILE REFERENCE: 01997.027701
CURRENT EPPLICATION NUMBER: US/11/128,061
CURRENT FILING DATE: 2005-05-11
CURRENT FILING DATE: 2005-05-11
PRIOR APPLICATION NUMBER: US 60/570,425
PRIOR PILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
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APPLICANT:
APPLICANT:
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ORGANISM: Mesocricetus auratus FEATURE:
                                         TYPE: DNA
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                                                              ENGTH: 1234
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Local Similarity 56.7%;
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Hann, Louane E.
Sinacore, Martin S.
Leonard, Mark W.
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Mounts, William M.
                                                                                                                                                                                                                                                                                                                                                         Sinacore, Martin S.
Leonard, Mark W.
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Pred. No. 0.031;
Pred. No. 0.031; Indels
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US-11-128-049-869
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RESULT 12
US-11-128-049-4511
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LOCATION: (876)...(891)
OTHER INFORMATION: n is
US-11-128-049-869
                                                                                                                                                                                                                                                                                               Best Lou-
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Best Local Similarity
Matches 97, Conserv
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APPLICANT: Leonard, Mark W.
APPLICANT: Brown, Eugene L.
APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
TITLE OF INVENTION: MAKING AND USING SAME
FILE REFERENCE: 01997.027700
CURRENT APPLICATION NUMBER: US/11/128,049
CURRENT FILING DATE: 2005-05-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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Local Similarity 56.7%;
es 97; Conservaring
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llarity 56.7%;
Conservative
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Pred. No. 0.031;
0; Mismatches 74;
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APPLICANT: SINACOTE, MATCH S.
APPLICANT: Brown, Bugene L.
APPLICANT: Hoonard, Mark W.
APPLICANT: HILLER CONTINUED POLYNUCLEOTIDES RELATED TO TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO TITLE OF INVENTION: TO MONITOR GENE EXPRESSION FILE REFERENCE: 01997.027701
FILE REFERENCE: 01997.027701
CURRENT APPLICATION NUMBER: US/11/128,061
CURRENT FILING DATE: 2005-05-11
PRIOR APPLICATION NUMBER: US 60/570,425
PRIOR FILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
SOFTWARE: Patentin version 3.3
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APPLICANT: Leonard, Mark W.
APPLICANT: Brown, Eugene L.
APPLICANT: Miller, Christopher P.
APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: OLIGONUCLECTIDE ARRAYS TO
TITLE OF INVENTION: MAKING AND USING SAME
TILE REFERENCE: 01997.027700
CURRENT APPLICATION NUMBER: US/11/128,049
CURRENT APPLICATION NUMBER: US 60/570,425
PRIOR PILING DATE: 2004-05-11
PRIOR FILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
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TYPE: DNA
ORGANISM: Mesocricetus auratus
PEATURE:
NAME/KEY: misc feature
LOCATION: (876)..(891)
                                             SEQ ID NO 6860
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TYPE: DNA
                   ENGTH: 600
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Mounts, William M.
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Mounts, William M.
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Pred. No. 0.031;
0; Mismatches 74;
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ORGANISM: Cricetulus griseus

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RESULT 15
US-11-128-061-3218
US-11-128-061-3218
; Sequence 3218, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
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US-11-128-049-6860
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PRIOR FILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
SOFTWARE: PatentIn version 3.3
SEQ ID NO 6860
LENGTH: 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6860, Application US/11128049 Publication No. US20060010513A1 GENERAL INFORMATION:
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Best Local (
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Best Local Similarity 55.6%;
Matches 100; Conservative
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TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO
TITLE OF INVENTION: MAKING AND USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 01997.027700
CURRENT APPLICATION NUMBER: US/11/128,049
CURRENT FILING DATE: 2005-05-11
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APPLICANT: Charlebois, Timo
APPLICANT: Mounts, William!
APPLICANT: Hann, Louane E.
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Leonard, Mark W.
Brown, Eugene L.
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Pred. No. 0.033;
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Pred. No. 0.033;
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